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OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:02:50 ; Search time 6647.57 Seconds
(without alignments)
11867.952 Million cell updates/sec

Title: US-09-787-657-3
Perfect score: 3770
Sequence: 1 tactatagggcgccgcgaa.....aaaaaaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 5595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Geneml: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
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12: gb_sy: *
13: gb_un: *
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22: em_ov: *
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27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3288.2	87.2	3464	9	HSAT272213	AJ272213 Homo sapi
5	3166.6	84.0	3213	6	AX098884	AX098884 Sequence
6	3166.6	84.0	3213	6	AX099304	AX099304 Sequence
7	3113.6	82.6	3114	6	AX098883	AX098883 Sequence
8	3113.6	82.6	3114	6	AX099303	AX099303 Sequence
9	3056.6	81.1	3057	6	AX098882	AX098882 Sequence
10	3056.6	81.1	3057	6	AX099302	AX099302 Sequence
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14	1197.4	31.8	3339	6	AX098927	AX098927 Sequence
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ALIGNMENTS

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DEFINITION	AX098896					
ACCESSION	AX098896.1	GI:13538125				
VERSION						
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ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
BASE COUNT						

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Location/Qualifiers

1..3770

/organism="Homo sapiens"

/db_xref="taxon:9606"

WARNER-LAMBERT COMPANY (US)

Patent: WO 0119870-A 21 22-MAR-2001;

same

calcium channel subunit polypeptides and screening assays using

Brown,J.P. and Bertelli,F.

1 (bases 1 to 3770)

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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VERSION	AX099316.1 GI:13538471		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 3770)		
	Bertelli,F., Brown,J.P., Dissanayake,Y., Suman-Chauhan,N. and		
	Gee,N.S.		
TITLE	Screening for alphasdelta-1 subunit binding ligands		
JOURNAL	Patent: WO 0120336-A 21 22-MAR-2001;		
FEATURES	WARNER-LAMBERT COMPANY (US)		
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ACCESSION AJ272268
VERSION AJ272268.1 GI:7105925
KEYWORDS calcium channel alpha2-delta3 subunit.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3544)
AUTHORS Hanke,S., Bugert,P., Chudek,J. and Kovacs,G.
TITLE Cloning a calcium channel alpha2delta3 subunit gene from a
putative tumor suppressor gene region at chromosome 3p21.1 in
conventional renal cell carcinoma
JOURNAL Gene 264 (1), 69-75 (2001)
MEDLINE 21142395
REFERENCE 2 (bases 1 to 3544)
AUTHORS Kovacs,G.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Kovacs G., Department of Urology,
University of Heidelberg, Laboratory of Molecular Oncology, Im
Neuenheimer Feld 365, Heidelberg, 69120, GERMANY
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VERSION	AJ272213.1							
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1 (bases 1 to 3464)							
TITLE	Hanke, S., Bugert, P., Chudek, J. and Kovacs, G.							
JOURNAL	Cloning a calcium channel alpha2delta-3 subunit gene from a putative tumor suppressor gene region at chromosome 3p21.1 in conventional renal cell carcinoma							
FEATURES	Gene 264 (1), 69-75 (2001)							
SOURCE	2 (bases 1 to 3464)							
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	Direct Submission							
	Submitted (17-FEB-2000)							
	Kovacs G., Department of Urology,							
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 3213) Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and Gee, N.S.
TITLE	Screening for alpha2delta-1 subunit binding ligands
JOURNAL	Patent: WO 0120336-A 9 22-MAR-2001;
FEATURES	WARNER-LAMBERT COMPANY (US)
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REFERENCE 1 (bases 1 to 3114)
AUTHORS Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and Gee, N.S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 8 22-MAR-2001.
WARNER-LAMBERT COMPANY (US)
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Query Match 82.6%; Score 3113.6; DB 6; Length 3114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

LOCUS	DEFINITION	SEQUENCE	FROM	PATENT	WORLD	1987	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517
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[illegible]

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Db 781 GTGAGCTGACGTGACGACATGAAAGGACCTCGTGTGACTATCGGAGGCAAAAGCTGTCA 840
Qy 984 tcaatttggatacacttgggagtatgacttcttcaacataatgcttataatgagag 1043
Db 841 TCCATTTTGGATACACTTGGGGATGAGACTTTCTTCAACTTAATTTGCTTTAATGAGAG 900
Qy 1044 ctccacatgttggaaccttgcctgaatggaacttggctgaagccgacgaagaacaa 1103
Db 901 CTTCACATATGTGAACTTCTGTAATGAACTTTGTGTGAGCGCGACGACAAACAA 960
Qy 1104 gaagcacttcaggagacatctgcgaacaaacttgcgcaaaagaaatgtgaatgtatata 1163
Db 961 GAGACACTTCAGGGAGCATCTGGAACAACTTTTGCCAAAGGAATGTGAATGTGATATA 1020
Qy 1164 gctctgaatgaagccttcaacatcttgaatgtattcaacacagcgacgaagaaatc 1223
Db 1021 GCTCTGAATGAGCGCTTCAACATTTCTGATTTCAACACACAGGGACAAAGAAATATC 1080
Qy 1224 tggagtcaggccatcatgctcataactgatgagcggtggaacacttgaatacattt 1283
Db 1081 TGGAGTCAGGCGCATCATGCTCATTAAGTGGGGGTGGACACTTATGATACATCTTT 1140
Qy 1284 gcaaaatacaatttggccagatcgaaaggttcgcacttccacataccatcttgcagag 1343
Db 1141 GCAAAATACAAATGGCCAGATCGAAAGTTGCGATCTTCACATACCATTTGACGAGAG 1200
Qy 1344 gctgcgttgcagacaaatcctaaagtgaatggcctgtgcgaacaaagtatttaccag 1403
Db 1201 GCTGCGTTTGCACACATCTMAAGTGGATGGCTGTGCCAAACAAAGATTTTATCCAG 1260
Qy 1404 atctccaccttgcctgaatgtgcaggaagaatgtcatgaataccttgcgtgcttaagccg 1463
Db 1261 ATCTCCACTTGGCTGATGTGCGAGGAATGTCTGGAATTAACCTTCAACGTCCTTAAGCCGG 1320
Qy 1464 cccaaatgcacgacccagagacatgaatgtgtgcgacgaagcttcaatgcagcact 1523
Db 1321 CCCAAATCTCATCGACCGAGAGCATGATGTGTGGACCGAAGCTTCAATTGACAGCACT 1380
Qy 1524 ctgactgaatgaatcagggccccgctcctgaatgaacacatgtgaacagcctgtgttaag 1583
Db 1381 CTGACTGATATATCAGGGCCCGCTCTGATGACCACTGTACCAAGTCTGTGTTATGTAAG 1440
Qy 1584 cagaacgaacccagatcgaaagggatctctcctgagagtggttgcgacagatgtccagtg 1643
Db 1441 CAGAACGAACCCAGATGGAAGGCGATTTCTTGAGAGTGGTGGCAGATGTCTCCAGTG 1500
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Db 1501 AAAGAACTTCTGAAGACCATCCCAATATCAAGTTAGGATTCAGGTATGCTTTGCA 1560
Qy 1704 atcaacaaataatggtatatacctgcgaacatccggaactcaggtcgtcgtacgaagaaga 1763
Db 1561 ATACCAAAATATGATGRTATATCTGACCGCATTCGGAACCTCAGCGCTGTGCGAAGAGGA 1620
Qy 1764 aaaaaggaagaaacctaactaagtagaggttgaacctcctgagagtgaggttgaagagac 1823
Db 1621 AAAAAGGAAGGAACCTAATCTATAGTACGCTTACTCTGTAGGTGAGTGGGAAGAC 1680
Qy 1824 cgaagatgcgttgcgaanaatgtctatgtgaatcgaagaacgaggaagtttccatgag 1883
Db 1681 CGAGATGACGTGTGAGAAATGCTATGATGTAATGGAAGACGGGAGGATTTCCATGAG 1740
Qy 1884 gtaagaagaagcagtggaacaaaggaagcggttgcgtatgataacaaatgactactat 1943
Db 1741 GTGAAGAAAGACAGTGGCAAAAGGGAAACGGGTTTGTGATGACAAATGACTACTATTAT 1800
Qy 1944 acagacatacaggtactccttcaagttaggtgtgacgttccagaagtcacagggaaa 2003
Db 1801 ACAGACATTCAGGGTACTCTTTCAGTTTGTAGGTGGCGCTTTCCAGAGGTGATGGGAAA 1860
Qy 2004 taattcttcgaggaatgttaacatcgaagaagccttgatgaacttagaacatccgat 2063
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Db 1861 TATTTCTCCGAGGGAATGTAAACCATCGAAGAGCGCTGCATGACTTAAGAATCCGAT 1920
Qy 2064 gtgtcccttggagaatgaatgttcttactgcgaacctgaaccttaacctgaacccgat 2123
Db 1921 GTGTCTTGGCAGATGATGTCTTACTGCAACCTGACTACACACCTCGAGACCGCAT 1980
Qy 2124 ctgtcgaatgaagaagcattgaacttaacttaagaagcaagaacctctgcagtg 2183
Db 1981 CTGTCTCAGTTAGAAAGCATTAAGCTTACTTAAGGCAAGAAACCTCTCTCAGGT 2040
Qy 2184 gataaagaatltatcacaagaagtccttltgacgcygtgtgaagtcgcccatgtgaagcg 2243
Db 2041 GATAAAGAAATGTATGCAAGAAGTCTTTTGTGACCGGGTGTGAGTGGCCCCATTTGAAGCG 2100
Qy 2244 taattgacagccttgccttaacaaatctgaaatcttgcgaagggcgtgtgaagttg 2303
Db 2101 TATTGGACACACCTGGCGCTTCACAAATCTGAAATTTCTGCAAGGGCGTGTGAGGTTGCC 2160
Qy 2304 ttcttcggaacttgcagggccttccagaatcaacctgttgcggggcgtgagcagctc 2363
Db 2161 TTCTCTGGCACTCCGACGCGCTCTCCAGATCAACCTGTTTGTGCGGGCTGACAGCTC 2220
Qy 2364 accaatcaggaacttccctgaagaagctgcgacgaagagaacatlttlaacgcagacatctc 2423
Db 2221 ACCAATGAGGACTTCTGAAAGCTGGCGACAAAGGAACATTTTAAAGCGACACATTTTC 2280
Qy 2424 cctctctgtatcgaagaagccgctgcagcagaatccgaaggagcttgcctactgaatccca 2483
Db 2281 CCTCTGTGTAACCAAGCGCGCTGACAGATTCAGAGGACCTTCTGCTACTCATCCCA 2340
Qy 2484 ttccagcacttgcagcagatcaaaagaagatgtgtgaagaagaatgtatcatccagctc 2543
Db 2341 TTCAAGCATGACCAAGATCAATTAAGCATGTGTGTGACAGCAAGTACATCCATCAGCTC 2400
Qy 2544 ctgatagaacggaatcctcctgtgtgcgagctgtlaaggtcattcagatgaacttgaatt 2603
Db 2401 CTGATGAAACCGAATCTCTGTGTGTGACAGCTGATGAGCATTCAGATGAATCTGAATTT 2460
Qy 2604 ttccaagaagaatcttgcagcgcagcagaagaagtgcttccctcgatggaatgtctcc 2663
Db 2461 TTCCAAGGAAGTTCTGTGACCTGCCAGCAGACAGTGTCTTCCGTGAGAGGCAAAATGTCTCC 2520
Qy 2664 atccagctgtgaatgaatgaagcgtgaatgttacttcaatgaagaataatgtatatttg 2723
Db 2521 ATCAAGCTGTGATGATGAGACCTGTGAATTTACTCTAAGACATTAATGATTAATTTTG 2580
Qy 2724 gtgtcgaagaactacacacagaactggaacttlttgtgtgaatcgaagagcgtgtga 2783
Db 2581 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGATGAGAGGAGCTGTGATG 2640
Qy 2784 aacaatltgtcaacaatgtgggtcctttaaagaattaccctttagacttaaccaagcatg 2843
Db 2641 AACAAATTTGCTAAACAAATGGGCTCTTTAAAGAAATTAACCTTTATGATACCAAGCCATG 2700
Qy 2844 tgtagagccaaacgaagaagaagcagatgtgcgccaatggccccggatccctataatg 2903
Db 2701 TGTAGAGCCAAAGGAAGAGGATGCGCCCATGGCTCTGTGATCCTTAATATGCC 2760
Qy 2904 ttctctctgcagtaaaatgtgaatcagaagaacttgcctgttctcgtgtgtgaattaa 2963
Db 2761 TTCTCTCTGACGATTAATGATCATGACAGAACTTGTCTGTGCTGTGATTTAAAC 2820
Qy 2964 ctctgcaggttgtgtgacatccgatatagcagctaaagcccaagaatltgaacaagacctg 3023
Db 2821 CTGTGCAAGTTGTGTGCACTCGATATGACACTTAAAGCCCAAGAAATGAAACCAACCTG 2880
Qy 3024 gaggctgtgatactgaatataccagatctgtcctgtagcgcacacatcaagaagactata 3083
Db 2881 GAGCCTGTGTATCTGAATATCAAGCATGTGCTCTGTAGCGCCACATCAAGAAATCA 2940
Qy 3084 gggataatltgctgtgaagaactgtccaagtccttgtcatccagaacaaatcccaagc 3143
Db 2941 GGAATATTTGCTGTGAAGACTGCTCAAGTCTTGTGATCCAGCAAAATCCCAAGCAGC 3000
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QY	1824	cgatgacgctgtttggaaatgctatgtagaaatcgaaagacggggaaatttccatgag	1883
Db	1681	CGAATACAGCTGTGTGGAAATGCTATAGTGTAATCGAAAGACGGGAAATTTTCCATGGAG	1740
QY	1884	gtgaagaagacagtggacaaagaaacgggttttggtgatgacaaeagcatctatat	1943
Db	1741	GTGAAGAAGACAGTGGACAAAGGAACGGGTTTTGGTGATGACAAATGACTACTATTAT	1800
QY	1944	acagacatcaagggtatctcccttcagtttagtgtagcgctttccaaagttcatgaggaa	2003
Db	1801	ACAGACATCAAGGCTACTCCTTTACATTTAGGTGTGGCGCTTTCCAGGTGATGGGMAA	1860
QY	2004	tattcttcgaggagatgtaaccaacgaaagagccgcagatgacttagaacatcccat	2063
Db	1861	TATTCTTCCGAGGAGATGTACCATTCGAAGAAAGCCCTGATGACTTGTGAACATCCGAT	1920
QY	2124	ctgtctacagttaagaacgattaaagctctccctcaaaaggcaagaaacctctctcaggt	2183
Db	1981	CTGTCTACGTTAAAGAGGATTAAAGCTCTACCTPAAAGGAAAGAAACCTCTGCTCCAGGT	2040
QY	2184	gataaagaatttgaatccaaagaagtccttttgacgcggtgtagtgcctccattgaaagc	2243
Db	2041	GATPAAAGATTGATTCACAAAGAAAGTCCTTTTGAACGGGGTGATGATGCCCATTTGAAGCG	2100
QY	2244	tattggaccagcgtctggtccttcaacaaatctgaaaatctgacaaggtgcgtggaagttgc	2303
Db	2101	TATTGGACCAAGCTGGCCCTCAACAAATGTGAAATTTGACAAAGAGTGATGAGAGTTGCC	2160
QY	2304	ttccctcgacatcgacacggccctcccaagaatacaaccgtttgttcggtgcgacagctc	2363
Db	2161	TTCTCGGACACTGGACAGGGCCCTCTCCAAATCAACACTTGTGTGCGAGCTGAGCAGTCC	2220
QY	2364	accaatcaggacttctctgaaagctgtgcgaagaagaaacattttaacgacacatttc	2423
Db	2221	ACCATATCAGACATCTCTGAAAGCTGGCGCAAGAGGAACATTTTAAAGCAGACCATTTTC	2280
QY	2424	ccctctcgtgtaacgaaagacggcttgagagattccaaggagatttgcctatgatalcca	2483
Db	2281	CCTCTCTGGTACCGAAAGAGCGCTGTGACAGATTTCAGGGAGGCTTGCTGTACTCGATCCCA	2340
QY	2484	ttcagcacctgagcacgttcaataaaagcaatgtgtgtgacagcaagta>ttcaatcacgtc	2543
Db	2341	TTGACGACTGGACACGATCAATAAAGCATGTGATGACAGCAAGTATTCATCCAGTCC	2400
QY	2544	ctgtagtaaacgggaaatctctctgtgtgtgcacgtgtgaagcatctcagaatgaactgaaatc	2603
Db	2401	CTGTGATTAACGGAAATCTCTCTGTGTGGAGAGCTGTGAGGATTTCAAGATTTGAATTT	2460
QY	2604	ttccaaaggaagttctgagactgtgcacacagatgtgtctccctgtgtgacaaatgtccc	2663
Db	2461	TTCCAAAGGAAGTTCTGAGACTGGCACTGACACAGTGTGTCTCCCTGTGATGGCAATGTCCC	2520
QY	2664	atcagcgtgtagtagagactgtgaaatgtgttaacctaatagacaataatgatatatttg	2723
Db	2521	ATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATGACAAATAAAGGATTTATTTTG	2580
QY	2724	gtgtcgtgaagacatacacaacagacttgtagactttttgttgtagatcgaaggagctgtgagt	2783
Db	2581	GTGTCTTAACACTACACACAGACTGGAGACTTTTTTGGTGAATGTGAAGGAGAGCTGTGATGT	2640
QY	2784	aacaacatgtctaaacaatbvggcttcctttaaagaatatacccttatagactaacaaagcatg	2843
Db	2641	AACAATATGCTTAACAATAGGCTCTCTTTAAATAAATAATACCTTTATGACTACCAAGCCATG	2700
QY	2844	tgtagagccaacaaagaagacagcgatggtgcgcacatggtcctctgtgacttccatataatggc	2903
Db	2701	TGTAGACCCAAACAAGAAAGACAGATGGCGCCCATAGGCGTCTCTGTGATCTTTATATATGCC	2760

[illegible]

	FSR"		
BASE COUNT	1017 a	876 c	938 g
ORIGIN			879 t

Query Match	78.48;	Score 2956.6;	DB 10;	Length 3710;
Best Local Similarity	88.58;	Pred. No. 0;		
Matches 3319;	Conservative	1;	Mismatches 370;	Indels 61; Gaps 8

[illegible]

OY	997	cacttgaggatagatgacttcttcaacaataatgtcttatataaagaagcttcaactatg	1053
Db	951	ctctgggggagatgagacttcttcaacatcattcagatataaacaaggcttctatgtgg	1010
OY	1057	aacctgtccbaayggaacttggctgaagccgaacgaagcaacaagaagcacttcag	1118
Db	1011	AACCTTGTCTAAGGGAACACTGGTTCAAGCTACAGGACCAACAGAGACACTTCAGG	1070
OY	1117	agcatctygacaacacttctcgccaagaaygaattgnaatgttggatataagcttgaatga	1176
Db	1071	AGCATTTTGGACAAACTTTTGGCCAAAGGATTTGGATTTGCTGATATTCGACTGAGCAGG	1130
OY	1177	ccctcaaacatctcgaatgatttcaaccacaggaagaagtatctgcagtcagcca	1236
Db	1131	CCCTTCACATTCATGAGGATTTTCAACCCACTGTGACAAAGGAAGCATTTTGACCCAGGCCA	1190
OY	1237	tcatgtcatbaactgaatgagggcggttggaacctatgaatactcttgcgaatacaat	1296
Db	1191	TCATGCTCATACTGATGGGGGAGGTGACACCTATATACCATCTTTGGAAATATTAAT	1250
OY	1297	ggccagatcgaagaagcttcgaatcttcaacatactcaatgaagaagcgctgcgttgcag	1356
Db	1251	GGCCAGACCGAAAGCTTCGAATCTTTACTTACTCTATTTGAGAGGAGGCTGCTTTTGGCG	1310
OY	1357	acaaatcaaatgtgaatgagcctgtgcacaacaagaattttaaaccagaatctccactt	1416
Db	1311	ACAATTCACATGATGATGGCTGTGTGCTACAAAGATTTTTCACCCAGATCTCCACTTGG	1370
OY	1417	ctgatgtgcagggagaatgcatatgaatlaactcaagtgctgttggccggccaagaatcag	1476
Db	1371	CTGATGTGCAGGAAATGATATGATTAATCCATTCATGCTTATGCGGACCTTAAGCATTTG	1430
OY	1477	accagagacatgatgtgtgttgaccggaagcttacaatctaacagca-----	1522
Db	1431	ACCAAGAGCATGATGTGTGTGACCGAAGCGTACTTACAGCACCTCCCTCAGGCTC	1490
OY	1533	-----tctgaactgatcatcaggcccgctccctgaatgaacacgttagcaatgcgtgttta	1578
Db	1491	AAAACTTTCGTGAGATCAGAGGCGCTGCTGTATGACCCGCTGGCCATTCGCTGTGTTA	1550
OY	1579	gtaagcagaacgaacaacagatctgaagggatctctcttggagatgtgttgacaagatg	1638
Db	1531	GTAAGCGAAGACACTAGTCTCAAAAGGCAATTCCTTGTGGGTGTGGTGTGGACAGATGTC	1610
OY	1639	cagtgaaagacactctctgaagaacacatccccaatatagaatctlaagatctcaatgttgc	1698
Db	1611	CAGTTAAAGAGCTTCTGAAGACCATCCCAATATACAATGATTAGATTCATGGTACGCT	1670
OY	1699	tctgcaatcaacaataatgattatataccctgaacgcatcccggaactcaagctgctgtcaag	1758
Db	1671	TCGCGATCACGAAATAAATGATATATCTCTACAGCACCGGAGCTCAGGCACTGTATGAG	1730
OY	1759	aagaaagaagaagcaagaagaacccaactatagatagcgctgaacctctcgaagtgaagtgg	1818
Db	1731	AAGAAAAAAACGGAGGAACCCCACTACAGTATGATGTCTCTTAAGTCACAGTGG	1790
OY	1819	aagaacgagatgaacgttgtgaagaatcgtcatatggaatgaagaacgggggaatttcca	1878
Db	1791	AAGACCGGGATATGTGTTCAGAAATGGCATGTAAATCGAAGACGTGGAAATTTCTCA	1850
OY	1879	tgaaggtgaagaagacatggaacaagaaggaaacgggttctgtgtgaatgaacaaatgactact	1938
Db	1851	TGCAAGTGAAGAAGACCGTGTGACAAAGGGAACGGGTTTGGTGATGACCAATGACTACT	1910
OY	1939	attataaagcatcaaaaggtgtactcccttcaagtttagtggtgtgcgttctcaagagtcat	1998
Db	1911	ACTATACAGACATCAAGGGTACTCCCTTTTACGTTTAAAGTGTGGCGCTCCACAGGGCCATG	1970
OY	1999	ggaataatctctccgaagggaatgtaacacatcgaaagaagcgctgtgaatctagaacatc	2058
Db	1971	GGAATATCTTCTTCCAGGGAATGTATACCATTTGAAGAAAGGCTCCTCATGACTTAAACATC	2030
OY	2059	ccgatgtgtcctctgacagatgaatgtgttcttaactgcaacatgaaacttaaaccttgaac	2118

Db 2031 CTGACGTCCTTGCGACAGATGAATGTCCTACTGCAACACTGACCTCACCAGCAGCACC 2090
Qy 2119 gccctcgtctcgaattgaagcgaattgaagctctacccctaaaggaagaacctcgtcc 2178
Db 2091 GCCCTTCTCTCAACTGCAAGCCATTTAAAGCTCTACCTCAAGGCAAGCGCTGCTGCTTC 2150
Qy 2179 agtctgaataaagattgatccaagaagctctcttgacgcggtgtgtagtccccccattg 2238
Db 2151 AATGTGACAAAGAAATTTGATTCAGAAAGTCCCTTTTGTGATGCTGTGTGTAAGCCCTATTTG 2210
Qy 2239 aagcgtatctgaccagcagctcgtccctcaacaactctgaaactctgacaaagcgctgag 2298
Db 2211 AAGCCTATTGAGCAGAGCTGCGCTGCTCAACAATCTGAAATTTGAGCAAGGGTGAAGG 2270
Qy 2299 ttgctctccttcgacactcgcacgcggtctctcagaataacctgttgtcggtggtcagc 2358
Db 2271 TCGCCTTCTCTGCGACCTGCGCAGGCTCTCAAAATCAACCTGTGTGGGGCCGCAAC 2330
Qy 2359 agctcacaatcgaactctcctgaagctgagcgaagaagaaacatcttaacgcagacc 2418
Db 2331 AACCTCACCAATCAGACTTTTGTGAAGCTGAGACAAAGAAACATTTTAAATGCCGATC 2390
Qy 2419 attccctctctgttacgaagaagcgcgtgagcagattccagggagctcgtctactcga 2478
Db 2391 ATTTCCTCTCTGTGTAAGAGAGCTGCGCAGATGCGAGGAAGCTTGTGCTATTTCGA 2450
Qy 2479 tcccatcagcagctgagcaccgactcaataaagcaatgtgtgtacagcgaatcaccatcc 2538
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Qy 2539 agctcctgagatgaacggaatactcctgtgtgtgagcagctgtgagcagtcagatgaactg 2598
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Qy 3079 ctacagggaatattgtctgtgaagaactgctcgaagctcctgtcatccagaataatccaa 3138
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DEFINITION Sequence 51 from Patent WO0119870.
ACCESSION AX098926
VERSION AX098926.1 GI:13538143
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3209)
AUTHORS
Brown, J.P., and Bertelli, F.
TITLE
Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 or -g(a)2-g(d)-4
calcium channel subunit polypeptides and screening assays using
same

JOURNAL
Patent: WO 0119870-A 51 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
LOCATION/Qualifiers
SOURCE
1..3209
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 757 a 888 c 920 g 644 t
ORIGIN

Query Match 32.1%; Score 1211.6; DB 6; Length 3209;
Best Local Similarity 63.6%; Pred. No. 3.7e-234;
Matches 1932; Conservative 0; Mismatches 1069; Indels 39; Gaps 4;

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Qy 2515 tggtagaagaatgataccatccagctccctgtagaagaaatctcgttggtagaag 2574
Db 2443 TGGTAGACGGACAGACAGCTGTGGCGGTGAOCCTGGACAGAGAGACAGCCATTCTGCAG 2502
Qy 2575 ctgtgaagcattcagatgaactgaatttccaaaggaagttcgtgactgacagac 2634
Db 2503 CCGCGGGCGTCCAAATGAACCTGGAAATTCCTCCAGCCCAATTCGTGACCGCAGCGGCG 2562
Qy 2635 aggtgttcctccgtgagtagcgaatagtcctcaatcagctgtgtatgatactgtagattggtt 2664
Db 2563 AGTGCACAGCTGTGGATGGGCGCGTGACACAGAGACTCTGAGGACAGATGTGGACTGCT 2622
Qy 2695 acctcagaagaataatgataatttattggtgtcgtgaagactacacacagactggaact 2754
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Qy 2755 ttlttgtagatcagagagagctgtgataaacaattgctaacaatlyggtccttataa 2814
Db 2683 TTCTGGGGGAGGTGGATGATGTGTCTCTGACCCAGCTGCTCAGCATGAGGGGTTCAGCC 2742
Qy 2815 gaattacaccttataatgataccaagccatgtgttagagccaagaagaagacagcgaatgagc 2874
Db 2743 AAGGAGATATGATGATATCAGAGCCATGTGCAGAAACCTCGAGTCAACACACAGTGGAG 2802
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Qy 2995 -----ctaaagcccaagaattgaacagagacacctgtagacctt 3030
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Db 3163 CGACAGAAAGTCMAATATATATATCTCTGTCAATATGTGACCG 3202

RESULT 13
AX099346 3209 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 51 from Patent WO0120336.
ACCESSION AX099346
VERSION AX099346.1 GI:13538489
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3209)
Bertelli, F., Brown, J. P., Dissanayake, V., Suman-Chauhan, N. and
Gee, N. S.

TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 51 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
source location/Qualifiers
1. 3209
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 757 a 888 c 920 g 644 t
ORIGIN

Query Match 32.1%; Score 1211.6; DB 6; Length 3209;
Best Local Similarity 63.6%; Pred. No. 3,76-234;
Matches 1932; Conservative 0; Mismatches 1069; Indels 39; Gaps 4;

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Qy 310 ttgctgctaagtaactcgggtccagctctcgaagaataatataagaatgataagaaag 369
Db 223 CTGTGACCAATTACTCAAGGCTCTCTGTGTGCAGAAAGATACAGAGATGTGAGTCCA 282
Qy 370 acgttgcataagaagaattgagcctccaactgtgtaagaagctggccaagaacatgag 429
Db 283 GTCGTGAAGATGAGAGAGGTGATGCTTGAGAGCTGTGAGAGAGATTCACAGAGCATGG 342
Qy 430 aagagatgttcaacaagaagcttgagcgcgtcagcgctcgtgtgtaggctcagaagaag 489
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Qy 490 caacactgaacaagaatttgatgagactaagatagatgaatcactgaatgctgtgtcga 549
Db 403 CCGACTGAACACGAATTCATATGATCCCTGTGTTCGACTATTACACTGGGTCTGGA 462
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	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	(bases 1 to 3339)			
	Brown,J.P. and Bertelli,F.			
	Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4			
	calcium channel subunit polypeptides and screening assays using			
	same			
JOURNAL	Patent: WO 0119870-A 52 22-MAR-2001;			
	WARNER-LAMBERT COMPANY (US)			
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BASE COUNT	780 a 934 c 960 g 665 t			
ORIGIN				

Query Match	31.8%;	Score 1197.4;	DB: 6;	length 3339;
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OY	310	ttgcgtctaaagtactccgcggttcccaagctctctgcaaaagaatatacaagaagatctggaag	369
Db	223	CTGTACCAAAATATCTACGAGCTCTCTTGCTGCTCAGAGAGATACAAAGATGTGGAGTCCA	282
OY	370	acgttgcctatgaaagaattgatatgcccaccaactgtttaagaagctctgcaaaagaacatg	429
Db	283	GTCCTAGATCTCAGGAGAGGTGATGGCTTTGGACCTGTGATGAGAAAGTCTCAGAGGACATGG	342
OY	430	aagagatgttttacaagaagctctgagccgcgtcaagcgctctgctgctggaagctgcagaagaag	489
Db	343	AGAATCATGCTGGGGAGGAGAAAGTCAGGGGGGTCCAAATCTGGTGGAACTGCGCGAGGAGG	402
OY	490	caacacctgaacaatgaatttgatgcagacttaagtatgataacttcaatgctgtgtga	549
Db	403	CCGACCTTAAACCCACAAATTCATATGATCCCTGTGCTTGACATATTACACTGGGTCTCGGA	462
OY	550	taaatgaaaggagacaagcaggaattttcttgagctggaagaagaattcatcttagccc	609
Db	463	TCAAGGAGAGGGAGCCAGAAAGGCCAATCTCTGTGAGCTTGGCGCCGACATTTCTCTCGGAGT	522
OY	610	caaatgaccatttaataatttgcctgtgaaacatcagtctaagtgatgcgtlccaagiatcaa	669
Db	523	CCAAATGCTACACTTCAGCAACCTGCCGGTGAACACCTTCATCAGCAGCKGTGCGAGCTCCCA	582
OY	670	cgaatactgtacaacaagaacctgtaactgttcaatgggggttatattggtcttaactctcaa	729
Db	583	CCAAGCTGTACACAAACCAACCCAGATATTTTAAATGGAGTCTACATATCTGAAGCTTTGA	642
OY	730	acaaagtctttgtagataacttgaacgctlgacccaactctcatatgtagtactttgaa	789
Db	643	ATGCTGTCTTCGTGAGAGATCTCCAGAGAGACCCAACTTGACCTGCKCAATATTTTGGCA	702
OY	790	gtgcaaaaggcctttttagtcagtatccggggaattaaattggaaccacatagaattgag	849
Db	703	GTCGCAACTGGAATCTTTCAGGATCTTCCAGGATATTAATATGGACACCTGATGGAATGGAG	762
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AUTHORS			
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JOURNAL	Patent: WO 0120336-A 52 22-MAR-2001; WARNER-LAMBERT COMPANY (US)		
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RESULT 2
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ID AAS01414 standard; cDNA; 3770 BP.
AC AAS01414;
NC AAS01414;
DT 04-JUN-2001 (first entry)
XX Human secreted soluble alpha2delta calcium channel subunit #11 cDNA.
DE

```

XX Human: secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
XX filter binding assay; wheat germ lectin flashplate assay; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 144..3401
XX FT /tag=a
XX FT /product="Alpha2delta calcium channel subunit #11"
XX
XX MO200119870-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000: 2000MC-EP09137.
XX
XX 16-SEP-1999: 99US-0397550.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Brown JP, Bertelli F;
XX
XX MPI: 2001-235262/24.
XX
XX P-PSDB; AAU01024.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX flashplate assays, Nickel flashplate assays, Filter binding assays or
XX Wheat Germ Lectin flashplate assays -
XX
XX Claim 24: Page 93-94; 160pp; English.
XX
XX The present sequence encodes for human secreted calcium channel
XX alpha2delta subunit #11 which is soluble and retains the functional
XX characteristics of the full length or wild type alpha2delta subunit
XX (AAU01025) from which it is derived. The invention relates to truncated
XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
XX which retain their affinity for radioactively labeled gabapentin. The
XX alpha2delta subunit is 1 of the components of the heteromultimeric
XX voltage-dependent calcium channel (VDCC) complexes present in neuronal
XX and non-neuronal tissues including heart and skeletal muscle. Numerous
XX soluble forms of the human calcium channel alpha2delta subunits
XX (AAU01014-AAU01024 and AAU01037-AAU01038) and 5 soluble forms of the
XX poreine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
XX described. The secreted soluble alpha2delta subunit may be used in assays
XX e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
XX filter binding or wheat germ lectin flashplate assays to detect or
XX measure the binding or interaction of a ligand (e.g. gabapentin,
XX L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,
XX L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
XX alpha2delta subunit.
XX
XX Sequence 3770 BP; 1049 A; 871 C; 941 G; 908 T; 1 other;
XX
XX Query Match 100.0%; Score 3769.6; DB 22; Length 3770;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3770; Conservative 0; Mismatches 0; Indels 0; Gaps 0.0;
XX
XX 1 tactatagggcgccggaattcggcacagagcgcgagcgagcgagcgagcccgcg 60
XX |||||||
XX Db 1 tactatagggcgccggaattcggcacagagcgcgagcgagcgagcgagcgagcccgcg 60
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XX 61 ggcgtccgccacgcgcgcgtccgcgcagctcccgcgcgcgctctcgttcgcgcgcagc 120
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QY	241	cggagcaagagatcacgcctccgtcggagagctcctgcgcgtcttggtgggagaa	300
Db	241	cggagcaagagatcacgcctccgtcggagagctcctgcgcgtcttggtgggagaa	300
QY	301	taaaatccattcgtctgaagtaactcggcttcccaagctctcgcacaagaataacaaagagt	360
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QY	361	atgagaaagagcgtctgcctacaaagaaattgattgctcccaactcgtgtaaagagctgcgaa	420
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Dh	1261	tggacacctatgaatacaactcttgcacaataatacaatttggccaatcgaaggttcgcact	1320
QY	1321	tccataactcctatctgacaggaagcgttcgttgcagaacaactcaaaagtgaatggcctgtg	1380
Dh	1321	tccataactcctatctgacaggaagcgttcgttgcagaacaactcaaaagtgaatggcctgtg	1380
QY	1381	ccacaacaaagatttttaccacagatcccaacctgtgctgtagtgcagaagaattctactg	1440
Dh	1381	ccacaacaaagatttttaccacagatcccaacctgtgctgtagtgcagaagaattctactg	1440
QY	1441	aataccttcaactgtgtagccggcccaaaagtcatacgaccagaagcatalgatgtgtgtgga	1500
Dh	1441	aataccttcaactgtgtagccggcccaaaagtcatacgaccagaagcatalgatgtgtgtgga	1500
QY	1501	ccgaagcttcaacttgaacagatcctctgaactatgatacagggcccgctctgaatgcacactg	1560
Dh	1501	ccgaagcttcaacttgaacagatcctctgaactatgatacagggcccgctctgaatgcacactg	1560
QY	1561	taagcatgctgtgttagtaagaagcaagcaaacacagatcgaagggtaactctcttggagag	1620
Dh	1561	taagcatgctgtgttagtaagaagcaagcaaacacagatcgaagggtaactctcttggagag	1620
QY	1621	tggctggcacagatgttccacgtgaagaagacttctgaaagacatcccaaatatacaagttag	1680
Dh	1621	tggctggcacagatgttccacgtgaagaagacttctgaaagacatcccaaatatacaagttag	1680
QY	1681	ggattcaagttatgctcttgcacaatacaataatggtatatacccttgaagcattccggagac	1740
Dh	1681	ggattcaagttatgctcttgcacaatacaataatggtatatacccttgaagcattccggagac	1740
QY	1741	tcaagctgtgttgcagaagaaggaacaaagcgaaggaacaaactaactatagatgcgtttgac	1800
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Dh	1801	tctctcaggttgaagtgggaagaccgagatgaagctgttgaagaatgtctatgttgatcgaa	1860
QY	1861	agacgggggaagcttccatctgaagagtggaagaagcagctggaacaaagggaaacgggttttgg	1920
Dh	1861	agacgggggaagcttccatctgaagagtggaagaagcagctggaacaaagggaaacgggttttgg	1920
QY	1921	tgttgcacaatactgactatctatatacagacaaccaaggctactccttcaagtttaggttgg	1980
Dh	1921	tgttgcacaatactgactatctatatacagacaaccaaggctactccttcaagtttaggttgg	1980
QY	1981	cgcttccagaagtcatacgggaataatttcttccgagggaaatgttaaacatcgaaagagcc	2040
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Dh	2041	tgcatacttaagaacatcccgatgtgtctcttggcagatgaatgtgtcctactgcacaactg	2100
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Dh	2521	cagcaagtaacatccatccagctcctctgtgaatgaacgggaatctcctctgtgtggaagctgag	2580
QY	2581	gcattcagatgaacacttgaatttttccaaaaggaagttctggaacgtccagcgacagatgtg	2640
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QY	2641	cttcccttgaatgcaaatgtcctccatcagctgtgatagtgaagcgttgatgttaccctca	2700
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QY	3001	cccgaaattgaacacagaccccttgagccttgtgatacgtgaatatccagcatctgctctg	3060
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QY	3061	agcgacacatcaaggaagactacagggaaatattgcttgtgaagactgtcctcaagctcttg	3120
Dh	3061	agcgacacatcaaggaagactacagggaaatattgcttgtgaagactgtcctcaagctcttg	3120

[illegible]

PI	Johns MA, Moldover B, Oford JD:
XX	
DR	WPI: 2000-303744/26.
XX	
PT	New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT	proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT	anxiety, multiple sclerosis or cancer
XX	
P5	Claim 22: Page 85-86; 86pp: English.
XX	
CC	The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
CC	The gene has been mapped to chromosome 3p21.1. This gene and the related
CC	alpha-2-delta-D and -B genes are useful for protecting mammalian cells
CC	from abnormal calcium flux by introducing expression vectors containing
CC	the respective gene into mammalian cells. The antisense genes are also
CC	useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC	is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC	Therefore, alpha-delta-2 proteins may also be targeted to treat
CC	seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC	pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC	multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC	addiction syndromes, mood, depression or cancer.
XX	
SQ	Sequence 3598 BP; 1004 A; 836 C; 904 G; 853 T; 1 other;

[illegible]

Query Match	90.2%	Score 339.2	DB 21	Length 3596	
Best Local Similarity	95.3%	Pred. No. 0			
Matches 3594	Conservative	0	Mismatches 4	Indels 172	Gaps 2
Qy	1	tactatagggcgagccgaattctgcacagagggcgagcgagcagagcaagccgc	60		
Db	1	tactatgggagcgcggaattcgcacagagggcgagcgagcagagcaagccgc	60		
Qy	61	ggcgtgcaccaagccgcgtccgcgagctcccccgggscgtctcgtccgcgcgaag	120		
Db	61	ggcgtgcaccaagccgcgtccgcgagctcccccgggscgtctcgtccgcgcgaag	120		
Qy	121	gggagcgctggagggagaccagatgacgggcggggtctgcgcgcgcgcggtccggg	180		
Db	121	gggagcgctggagggagaccagatgacgggcggggtctgcgcgcgcgcggtccggg	180		
Qy	181	ggagctcgagctctcgtccgcgctctctacgcccgcgttgaggagacgtgtgacct	240		

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RESULT      4
AAA09261
ID          AAA09261 standard; cDNA; 3598 BP.
XX
XX
AC          AAA09261;
XX
DT          10-AUG-2000 (first entry)
XX
DE          Human alpha-2-gamma-C gene splice variant.
XX
KW          alpha-2-gamma-C; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
KW          anticonvulsant; antimigraine; antiparkinsonian; antidepressant;
XX          splice variant; ss.
XX
OS          Homo sapiens.
XX
XX          WO200020450-A2.
XX          13-APR-2000.
XX
XX          07-OCT-1999; 99WO-US23519.
XX
XX          07-OCT-1998; 98US-0103122.
XX          30-OCT-1998; 98US-0106473.
XX          29-DEC-1998; 98US-0114088.
XX
XX          (WARN ) WARNER LAMBERT CO.
XX

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[illegible]

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Db	1081	tgcsagtcagggccatcagtctacataactgtgatgggcggtgagacactatgataaactctt	1140
OY	1284	gcaaaatatacaatttggccaagtctgaagaaggttgcgacttccaactaccatcttgagcagag	1343
Db	1141	gcaaaatatacaatttggccaagtctgaagaaggttgcgacttccaactaccatcttgagcagag	1200

[illegible]

Db	2281	ccctcctcgtgtaccgaaagagccgctctgagcagatctccagggagcttcgtctactcgatccca	2340
QY	2484	ttcagcacctggaacagtcacaaataaagcaabtgctgacacagacatataccatccagctc	2543
Db	2341	ttccagcacttgagaccagacacaaataaagcaabtgctgacacagacatataccatccagctc	2400
QY	2544	ctggagctgaaacggaatctccctctggtgtgagcagctgtgagatccagatgaaactgtgaatt	2603
Db	2401	ctggagctgaaacggaatctccctctggtgtgagcagctgtgagatccagatgaaactgtgaatt	2460
QY	2604	ttccaaaggaagatctctgagactgcagacagatgctgtccctctggaatgagcaatgtgtcc	2663
Db	2461	ttccaaaggaagatctctgagactgcagacagatgctgtccctctggaatgagcaatgtgtcc	2520
QY	2664	atccagctgtgatactgagactgtggaattgtttacctcataagacaataatggaattattcttg	2723
Db	2521	atccagctgtgatactgagactgtggaattgtttacctcataagacaataatggaattattcttg	2580
QY	2724	gtgtctcgaagacatcacacacagactctggaagactttttgtgtggaatctgaaagggcctgtgag	2783
Db	2581	gtgtctcgaagacatcacacacagactctggaagactttttgtgtggaatctgaaagggcctgtgag	2640
QY	2784	aacaaatctgtcaacaatctggtctcccttaaaagaaatataccctttatgtactaccaaagcatg	2843
Db	2641	aacaaatctgtcaacaatctggtctcccttaaaagaaatataccctttatgtactaccaaagcatg	2700
QY	2844	ctgtgagagccaaacgaaggaagacagctgagctggcccaatgagctctctgtgactctataatgtcc	2903
Db	2701	ctgtgagagccaaacgaaggaagacagctgagctggcccaatgagctctctgtgactctataatgtcc	2760
QY	2904	ttctcctctcgcagatbaaaatggaatcatgtgaagaagaactgtctctgttccctgtgtggaatttaac	2963
Db	2761	ttctcctcctcgcagatbaaaatggaatcatgtgaagaagaactgtctctgttccctgtgtggaatttaac	2820
QY	2964	ctctcgcagatctgtgtgagcctctccgataagacagctctaaagccacgaagaatttgaacagagacttg	3023
Db	2821	ctctcgcagatctgtgtgagcctctccgataagacagctctaaagccacgaagaatttgaacagagacttg	2880
QY	3024	gagcctctgtgataactgtgaatactccagacatctgtctctgtgagcgcacacatacaagagagactaca	3083
Db	2881	gagcctctgtgataactgtgaatactccagacatctgtctctgtgagcgcacacatacaagagagactaca	2940
QY	3084	ggggaatatctgtctgtgtgaagacctgtccaaagctccctctgtcatactccagcaaatccccaagcagc	3143
Db	2941	ggggaatatctgtctgtgtgaagacctgtccaaagctccctctgtcatactccagcaaatccccaagcagc	3000
QY	3144	aacactgtctcatgtgtgtgtgtgtgagacagacagctgtccctctgtggaattctgtgtggcccatcaac	3203
Db	3001	aacactgtctcatgt	3060
QY	3204	atgtgaccccatctgaaatactgataataatgaatcccttaagctgtgtgaacgtctaa-----	3256
Db	3061	atgtgaccccatctgaaatactgataataatgaatcccttaagctgtgtgaacgtctaa-----	3120
QY	3257	-----ggccccaaggaagatccagaagggccccaagaattctgtgtcatagtttccatctc	3305
Db	3121	aaagatcagaagggccccaaggaatcagaagaagggccccaagaattctgtgtcatagtttccatctc	3180
QY	3306	gagagagaatgcaagggagatctgt	3338
Db	3181	gagagagaatgcaagggagatctgt	3213
RESULT	6		
AAFS7546	AAFS7546	standard; DNA: 3213 BP.	
XX	AAFS7546;		
XX	11-JUN-2001	(first entry)	
DE	Human calcium channel alpha2delta subunit encoding DNA.		

XX		Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KM	nervous system disorder; pain; epilepsy; anxiety; human; ds.	
OS	Homo sapiens.	
XX	WO200120336-A2.	
PN		
XX	22-MAR-2001.	
PD		
XX	18-SEP-2000; 2000WO-EP09136.	
PF		
XX	16-SEP-1999; 99US-0397549.	
PR		
XX	(WARN) WARNER LAMBERT CO.	
PA	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS,	
XX	WPI, 2001-257902/26.	
PI	P-PsDB: AAB62243.	
DR		
XX		
PT	Competitive binding assay for screening ligands which bind a cerebral	
PT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit,	
PT	where the ligands identified are useful for treating disorders of the	
PT	nervous system, including pain -	
PS		
XX	Disclosure; Page 71-72; 158pp; English.	
CC	The invention relates to a new method for screening ligands which bind a	
CC	cerebral cortical voltage-dependent calcium channel alpha2delta subunit,	
CC	preferably alpha2delta-1 subunit. The method comprises contacting a	
CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand of	
CC	interest and a labelled compound which binds the subunit, followed by	
CC	measuring the level of binding of the labelled compound to alpha2delta-1	
CC	subunit. The method is useful for screening ligands, preferably	
CC	biologically active products that modulate a nervous system function,	
CC	which bind a cerebral cortical voltage-dependent calcium channel	
CC	alpha2delta-1 subunit. The ligands identified by the method are useful	
CC	for treating disorders of the nervous system, including pain, epilepsy	
CC	and anxiety. The present sequence represents a human calcium channel	
CC	alpha2delta subunit encoding DNA.	
XX		
SQ	Sequence 3213 BP; 894 A; 727 C; 824 G; 767 T; 1 other:	
	Query Match 84.0%; Score 3166.6; DB 22; Length 3213;	
	Best Local Similarity 99.4%; Pred. NO. 0;	
	Matches 3195; Conservative 0; Mismatches 0; Indels 18; Gaps 1	
OY	144 atgcccggcgccggcttcgcgcgcgcgcgcgcgtcccgagggggcttcgcttcgtcgc 203	
Db	1 atggccgcggcgccggcttcgcgcgcgcgcgcgcgtcccgagggggcttcgcttcgttc 60	
OY	204 ggcctctctaagccgcgcgttgggggaacgtggtgccttcggagcaagaataaccgtctcc 263	
Db	61 ggcctctctaagccgcgcgttgggggaacgtggtgccttcggagcaagaataaccgtctcc 120	
OY	264 gtgtgtaaacgttcgttgcccttcgttcgtttgtgtggagataaaatcatctgtcctaagtac 323	
Db	121 gtgtgtaaacgttcgttgcccttcgttcgtttgtgtggagataaaatcatctgtcctaagtac 180	
OY	324 tccggttcccgagcttcgttgaaaaagaatacaaaagatgatgaagaagcgttcctaatgaa 383	
Db	181 tccggttcccgagcttcgttgaaaaagaatacaaaagatgatgaagaagcgttcctaatgaa 240	
OY	384 gaatttgtatgacctcaacttgcataaagaagctgcgcaaaagaacaatgtaaagatgtttcac 443	
Db	241 gaatttgtatgacctcaacttgcataaagaagctgcgcaaaagaacaatgtaaagatgtttcac 300	
OY	444 aagaagctgaagccgtlcaagcgcgtctgtgtgtagagctgcagaaagaacacactgaagaac 503	
Db	301 aagaagctgaagccgtlcaagcgcgtctgtgtgtagagctgcagaaagaacacactgaagaac 360	

QY 504 gaatttgatgcagactacagtaagtaactcatgtctgtcgtatgaataatgaaggagac 563
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QY 684 aaagacccctgaatttgcatttgggttattgtctgaattcttaaaccaagttttgtta 743
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Db 541 aaagacccctgaatttgcatttgggttattgtctgaattcttaaaccaagttttgtta 600
QY 744 gataacttgaacggtgaccccatctcatalatgagcaactttggaagtgcgaaggcttt 803
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QY 804 tttagagagatgcaggtgaggttaaatgggaacagatgaagaatgagtcattgctctgcac 863
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QY 864 tgcagagacccgaataatgtatcatccagcagcaactcttcgaaagaacgtgtcatcttta 923
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Db 1081 tgcagtcagggccatcatgctcatataactgagtgggcggtgagcaactcttatacaaatcttt 1140
QY 1284 gcaaaatatacaatttggcagagatcgaaaggttcgcacatcttcaacataccatgtgagcgaag 1343
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Db 1861 tattctctcgaagggaatgtataccaatcgagaagaagcgtgcattgataagaatcccgat 1920
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Db	2641	aacaaattctgacaaatctgagccctctttaaagaattaccctttatgactaccagaagcctg	2700
Qy	2844	tgttagagccaaacagaaagcagcagctgagcccaatggcctctctgtgatacctataatgccc	2903
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RESULT 7			
AAS01408			
ID	AAS01408 standard; cDNA: 3114 BP.		
XX	AAS01408:		
AC			
XX			
DT	04-JUL-2001 (first entry)		
XX			
DE	Human secreted soluble alpha2delta calcium channel subunit #5 cDNA.		
XX			
KW	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;		
KW	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;		
KW	gabapentin; scintillation proximity assay; SPA; nickel flashplate assay		
KW	filter binding assay; wheat germ lectin flashplate assay; ss.		
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OS	Homo sapiens.		
XX			
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FT	/note= "This sequence lacks a stop codon"		
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XX	WO200119870-A2.		

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Db 481 aataattgccttggaacatgaagtcataagtagcttccaagtccaacgaactgtacaac 540
QY 684 aaagaacctgcaattgtccaatgggtttattgtgtgaattcctaacaagttttga 743
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QY 744 gataacttgaacgttgacccactctcatatgtagcaatttggaaatgcaaaaggcttt 803
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QY 864 tgcaggaacggaaaatggtataatccagcgcaactctccgaaaagtcgtcaatttta 923
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RESULT 10
AAFS7544 standard; DNA: 3057 BP.
ID AAF57544
XX AAF57544;
AC AAF57544;
XX 11-JUN-2001 (first entry)
XX Human calcium channel alpha2delta subunit encoding DNA.
DE Human calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KM nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 1..3057
FT CDS /tag- a
FT MO200120336-A2.
PN 22-MAR-2001.
PD 18-SEP-2000; 2000MO-EP09136.
PF 16-SEP-1999; 99US-0397549.
PR (WARN) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
PI WPI: 2001-257902/26.
XX P-PSDB; AAB62241.
DR
XX Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit.
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
XX
XX Disclosure: Page 69-70; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit encoding DNA.
XX
XX Sequence 3057 BP; 848 A; 692 C; 778 G; 738 T; 1 other:

Query Match 81.1%; Score 3056.6; DB 22; Length 3057;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 tccggtcccaagctctcgcaaaaagaaatacaagaagatagagaagacgttgcataagaa 383
DB 181 tccggtcccaagctctcgcaaaaagaaatacaagaagatagagaagacgttgcataagaa 240
QY 384 gaattatgagcctcccaactcgtgtaagaagctgagcaagaatacgtgaagatgttccac 443
DB 241 gaattatgagcctcccaactcgtgtaagaagctgagcaagaatacgtgaagatgttccac 300
QY 444 aagaagctcgaagcgcgtcgaagcgtcgtggaagcgtcgaagaagcgcgtcgaagaacat 503
DB 301 aagaagctcgaagcgcgtcgaagcgtcgtggaagcgtcgaagaagcgcgtcgaagaacat 360
QY 504 gaattatgagcctcccaactcgtgtaagaagctgagcaagaatacgtgaagatgttccac 563
DB 361 gaattatgagcctcccaactcgtgtaagaagctgagcaagaatacgtgaagatgttccac 420
QY 564 aagaagcggaaatttttggagcgtggaagaagaaatcctcctagcccaaatgacatttc 623
DB 421 aagaagcggaaatttttggagcgtggaagaagaaatcctcctagcccaaatgacatttc 480
QY 624 aataattgctcgtgaaacacacagctcgaagctcgaagctcgaagctcgaagctcgaagct 683
DB 481 aataattgctcgtgaaacacacagctcgaagctcgaagctcgaagctcgaagctcgaagct 540
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DB 541 aagaagcctgcaattgcaatlgggttatttgcgtgaatcctcctaaacaaagtatttga 600
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DB 601 gataacttgacggtgacccatctcctatctatgacgaacttggagatgcaaaagcgtt 660
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QY 1044 ctccactatgtgaaacctgctcgtgaatggaacttggcgaagcgaagaacaaacaa 1103
DB 901 ctccactatgtgaaacctgctcgtgaatggaacttggcgaagcgaagaacaaacaa 960
QY 1104 gaagcactcgaagacatcgcgaacaaacttgcgaagaagaaattggaattggaatata 1163
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DB 1141 gcaaaataacatctgccaagtcgaagtggaagtggtcgaattcgaataactcattggaagag 1200
QY 1344 gctcgtcttgcagaacatcctcaaaagtgaatgagcgttgcgaacaaagatttttaccag 1403
DB 1201 gctcgtcttgcagaacatcctcaaaagtgaatgagcgttgcgaacaaagatttttaccag 1260

QY	1404	atctccacccttggtcgatgctgacgaggaatgctcatgtgaataccttcacgctgcttagccgg	1463
Db	1261	atctccacccttggtcgatgctgacgaggaatgctcatgtgaataccttcacgctgcttagccgg	1320
QY	1464	cccaaaagcatcgccaggaagcatgatgtgtgtgacccgaagtttaattggaagacct	1523
Db	1321	cccaaaagcatcgacacgaagacatgatgtgtgtgacccgaagtttaattggaagacct	1380
QY	1524	ctgactgtgatgacgagcccgctcctgtgatgacacgtgaacgacgctgtgttagtaag	1583
Db	1381	ctgactgtgatgacgagcccgctcctgtgatgacacgtgtgaacgacgctgtgttagtaag	1440
QY	1584	cagaaacgaacacagatcgaagggcatctctctggtgagtgtgtgacacgagtgtccagtg	1643
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QY	2244	tattggaacagcctgtgcccctcaacaaatctgaaaaattctgcaaggcgggtgagaattggcc	2303
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QY	2304	tctcctcgacatcgacagcgccctctccagaaatcaaacctgtttgtcgggtgacgagcagctc	2363
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QY	3024	gagccttgtgatactgaaatataccagatctgtctctgtgagcgacacatcaagagagactaca	3083
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QY	3084	gggaatatgtgtgtgtgaagaactgtctccaaagctccttgtgtatccagcaaatcccaagcagc	3143
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QY	3144	aacctgttcatagttgtgtgtgacacgaacgtcctctgtgaaatctgtgtgcccccatc	3200
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RESULT 11

AAA09260

ID AAA09260 standard; cDNA; 2008 BP.

AC AAA09260;

AC

AC

AC

DT 10-AUG-2000 (first entry)

DE Human alpha-2-delta-C gene 3' splice variant.

KW alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cytoskeletal;

KW anti-convulsant; antimitigrane; antiparkinsonian; antidepressant;

OS splice variant; ss.

OS Homo sapiens.

XX

<

DB 1681 ggattccggttatgcttccttgcaatccacaataatgatatatctctcagcattccggaac 1740
QY 1741 tcsagctgctgtacgaagaagaagaacgcaagaactaactatcgtagctgacc 1800
DB 1741 tcsagctgctgtacgaagaagaagaacgcaagaactaactatcgtagctgacc 1800
QY 1801 tctctgagtgagtgagtggaagaccgagatgactgtgtgaaatgctatggtgaatcgaa 1860
DB 1801 tctctgagtgagtgagtggaagaccgagatgactgtgtgaaatgctatggtgaatcgaa 1860
QY 1861 agacggggaagcttccatgagtgagtgagacagtgagcaaaagggaacgggttt 1917
DB 1861 agacggggaagcttccatgagtgagtgagacagtgagcaaaagggaacgggttttt 1917
RESULT 12
AAZ51626
ID AAZ51626 standard; cDNA; 1774 BP.
XX
AC AAZ51626;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human membrane channel protein-10 (MECHP-10) cDNA.
XX
KW Membrane channel protein-10; MECHP-10; diagnosis; treatment; lymphoma;
KW cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;
KW inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
KW diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
KW muscular disorder; myocarditis; Duchenne's muscular dystrophy; noctopic;
KW cardiovascular disorder; hypertension; bronchitis; vasculitis; candida;
KW neurological disorder; Alzheimer's disease; Parkinson's disease; human;
KW Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;
KW Anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
KW hypotensive; vasotropic; antiasthmatic; antiinflammatory; antidepressant;
KW anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..1742
FT FT /*tag= a
FT FT /product= "MECHP-10"
FT FT misc_binding 1275..1322
FT FT /tag= b
FT FT /bound_moiety= "Probe or Primer"
XX
PN WO200012711-A2.
XX
PD 09-MAR-2000.
XX
PE 02-SEP-1999; 99WO-US20468.
XX
PR 02-SEP-1998; 98US-0145815.
PR 12-NOV-1998; 98US-0191283.
PR 09-DEC-1998; 98US-0208821.
PR 26-JAN-1999; 99US-0237506.
PR 10-FEB-1999; 99US-0247891.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Bandman O, Tang YF, Reddy R, Hillman JL, Yue H;
PI Lal F, Corley NC, Guejler KJ, Gorgone G, Baughn MR, Azimzai Y;
XX
DR MPI: 2000-256643/22.
DR P-PSDB; AAY70460.
XX
PT Novel human membrane channel protein and polynucleotide useful for
PT diagnosing and treating cell proliferative, inflammatory, secretory,
PT osmoregulatory, muscular, cardiovascular and neurological disorders -
XX
PS Claim 9; Page 124-125; 140pp: English.

XX
CC The present sequence is a cDNA identified in Incyte clone 3148427
CC derived from ADRNON04 cDNA library. It encodes human membrane channel
CC protein-10 (MECHP-10), which is expressed in cardiovascular, endocrine
CC and nervous tissues. Anti-MECHP antibodies can be used as therapeutic
CC antagonists and reagents for diagnosis and monitoring diseases. MECHP
CC cDNA can be used for diagnosis of MECHP-related diseases and gene
CC mapping. MECHP can be used for treatment of cell proliferative disorders
CC such as bursitis and atherosclerosis, cancers like lymphoma and sarcoma,
CC inflammatory disorders like AIDS and Addison's disease, transport or
CC secretory disorders like cystic fibrosis and diabetes mellitus,
CC osmoregulatory disorders like diarrhoea and renal failure, muscular
CC disorders like myocarditis and Duchenne's muscular dystrophy,
CC cardiovascular disorders like hypertension and vasculitis, congenital
CC lung anomalies like bronchitis and asthma and neurological disorders like
CC Alzheimer's disease, Parkinson's disease and Huntington's disease.
XX
SQ Sequence 1774 BP; 539 A; 366 C; 440 G; 429 T; 0 other;
Query Match 41.0%; Score 1545; DB 21; Length 1774;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1614; Conservative 1; Mismatches 51; Indels 19; Gaps 2;
QY 252 ataccgcttcggtggtgaagctctgggcccgcgttctgtgtggggagataaacctt 311
DB 8 ataccggtgaccgcggtctgctgtaggaactcgggcgtcttggggagagaatac 67
QY 312 gctcctaagctacgcttccagctctcgaagaatcaagaagtagaagaagac 371
DB 68 catgctgaataaccggttccagctctcgaagaatcaagaagtagaagaagac 127
QY 372 gttccatagaaga-atgatgctcccaactggtlaaagaactgycaaacatgga 430
DB 128 gtgcctatagaagaactcgatggtcccaactggtlaaagaactgycaaacatgga 187
QY 431 agagatggttacaagaagcttgaggccgtgacgctgtgtgtagagtgagaagaagc 490
DB 188 agagatggttacaagaagcttgaggccgtgacgctgtgtgtagagtgagaagaagc 247
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DB 248 acacctgaacatgaattgtatgacacttacaatgaatgaatgaatgaatgaatgaat 307
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QY 671 gaacatgtacacaagaacccctgcaatgtlcaatgggggttattggttcgaatcctaa 730
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DB 488 caaagttttagataaacttgaacgctgacacatcttcataatggaactttagaag 547
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OY	430	aaggaatgtttcacagaagaatctcgaaagccggtccagagcgtctgtgttgagagctgcagaagaag	489
Db	341	agaacatgctgcgagaggaagatcgaaagcgggtccagaatctgtgttggaagctgcgcgaagag	400
OY	490	cacacgtgaacaacgaatctgtgatgcagactatcaatgaatgaatcttcacatgtctgtgcga	549
Db	401	cgcagccctggaacacgaatcttaacatgaaatccctgtgtgttcgactattacacctcgtccgga	460
OY	550	taaatgaaaggaacaagaacgagggaatttttttgagctgtggaagaaggaatctcatcttagccc	609
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OY	610	caaatgaccattttaaataatttcgtctgtgaacatcaagctctaaagtgaatcgtccaagtaacca	669
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OY	1270	atgatacaatcttggcaaaatacaatgtggccaacatctgaaagaagttcgcattcctcaataacc	1329
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QY	1684	ttcaaggttatgtcctttgcataccaataatgtgtatatctctgcagctgcgaactca	1743
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QY	1744	ggctgcctgcagaaagaaagaaacgcga--'gnaaaccttaactatagtcgtttgac	1800
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QY	1801	tctctgaagttgagttggaagaacccgagatgacgtgtgtagaatgtcatgtgtgactgaa	1860
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QY	1861	agacgggggaagtttcccatgtgggtgtgaagaagacagttgacaagaagggaacgggttttg	1920
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QY	1981	cgcttccagaggtcatgtggaataattctcttcgaagggaatgtatcaaccatcgaaagggc	2040
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QY	2041	tgcattgacttaaaatcccgaatgtgtcctctggcagatgaatgtgtcctactgcgaacctg	2100
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QY	2101	acctcaacccttagacacccgaactctgtctcgaatgtaagagcattaagttcactcaaaag	2160
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QY	2161	gcaaaagaactctgtctcagttgtgataaagaattgatccaaagaagttcctttttgacgg	2220
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Db 2441 tgggtgacggaagcacagcgtggtgacccgtgacaaagagacagccatctgctgcag 2500
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Oy 3349 ccacagaagatcctcctctcgtcctcctgt 3377
Db 3281 cctgcgcgcctcctacatctcgtgtgtgtgt 3309

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RESULT 14

AAA09254 standard: cDNA; 5073 BP.

AC AAA09254;

XX 10-AUG-2000 (first entry)

DE Human alpha-2-delta-D gene.

KW alpha-2-delta-D: calcium channel; 12p13.3; gabapentin; cytostatic;
 KW anticonvulsant; antimitigane; antiparkinsonian; antidepressant; ss.

```

OS Homo sapiens.
FX Key Location/Qualifiers
FH CDS 3..3365
FT CDS /tag= a
FT
PN WO200020450-A2.
PD 13-APR-2000.
XX
PF 07-OCT-1999: 99WO-US23519.
XX
PR 07-OCT-1998: 98US-0103322.
PR 30-OCT-1998: 98US-0106473.
PR 29-DEC-1998: 98US-0114088.
XX
PA (WARN ) WARNER LAMBERT CO.
PI
PI John MA, Moldover B, Offord JD:
XX
XX MPI: 2000-303744/26.
DR P-PSDB: AAY2321.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer
XX
XX
PS Claim 1, Page 64-66; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.
XX
SQ Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 other:

Query Match 33.6%; Score 1268.2; DB 21; Length 5073;
Best Local Similarity 63.6%; Pred. No. 1.2e-277;
Matches 2015; Conservative 0; Mismatches 1113; Indels 39; Gaps 4;

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Db 163 agatcctcttggaagaagtgaaagctatgtggtcgtgacccctgtgcggacctgtataaca 222
Oy 310 ttgtgtctgaagtaactcgtgtccagactctgtcaagaagaatacaagaagtatggaag 369
Db 223 cgtgtgacaaactcctaagctctctctgtgtcagagaagaatcacagatctgtgtgtcca 282
Oy 370 acgttgcataagaagaatgtatgtgctcctcaactgtgtaagaagctgtgcaagaatctg 429
Db 283 gtctgaagatcgaagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 342
Oy 430 aagagatgttctcaagaagcttgagccgtcagcgctcgtgtgtgtgtgtgtgtgtgtgtgt 489
Db 343 agaacatgtctgtggaagagtcgaagcggtcgaagatcgtgtgtgtgtgtgtgtgtgtgtgt 402
Oy 490 caaacctgaacatgaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 549
Db 403 ccgaacctgaacacgaattcaatgataatccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 462
Oy 550 taatgaagggacaaagcgggaatttctgtgagctgtggaagaaagaaatcatcatcagccc 609
Db 463 tcaacgagagggagcagagaagggcaactctgtgtgagctgtgtgtgtgtgtgtgtgtgtgt 522

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:12:30 ; Search time 125.14 Seconds
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Perfect score: 3770
Sequence: 1 tactatagggcgccgcgaa.....aaaaaaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	130.6	3.5	3566	1 US-07-745-206A-24	Sequence 24, Appl
2	130.6	3.5	3566	2 US-08-311-363-24	Sequence 24, Appl
3	130.6	3.5	3579	1 US-08-455-543A-36	Sequence 36, Appl
4	130.6	3.5	3579	2 US-08-193-078B-25	Sequence 25, Appl
5	130.6	3.5	3579	2 US-08-223-305C-36	Sequence 36, Appl
6	130.6	3.5	3579	3 US-08-949-386-32	Sequence 32, Appl
7	130.6	3.5	3579	4 US-08-450-562-32	Sequence 32, Appl
8	130.6	3.5	3579	4 US-08-984-709A-32	Sequence 32, Appl
9	130.6	3.5	3600	1 US-08-455-543A-33	Sequence 33, Appl
10	130.6	3.5	3600	1 US-08-455-543A-33	Sequence 33, Appl
11	130.6	3.5	3600	2 US-08-193-078B-11	Sequence 11, Appl
12	130.6	3.5	3600	2 US-08-223-305C-11	Sequence 11, Appl
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14	130.6	3.5	3600	2 US-08-149-097D-11	Sequence 11, Appl
15	130.6	3.5	3600	3 US-08-949-386-11	Sequence 11, Appl
16	130.6	3.5	3600	4 US-08-450-562-11	Sequence 11, Appl
17	130.6	3.5	3600	4 US-08-984-709A-11	Sequence 11, Appl
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19	130.2	3.5	3564	2 US-08-193-078B-24	Sequence 24, Appl
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21	130.2	3.5	3564	3 US-08-949-386-31	Sequence 31, Appl
22	130.2	3.5	3564	4 US-08-450-562-31	Sequence 31, Appl
23	130.2	3.5	3564	4 US-08-984-709A-31	Sequence 31, Appl
24	130.2	3.5	3585	1 US-08-455-543A-34	Sequence 34, Appl
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43	125.2	3.3	3802	1 US-08-435-675B-2	Sequence 2, Appl
44	125.2	3.3	3802	3 US-08-884-599-2	Sequence 2, Appl
45	125.2	3.3	3802	6 5386025-7	Patent No. 5386025

ALIGNMENTS

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RESULT 1
US-07-745-206A-24
: Sequence 24, Application US/07745206A
: Patent No. 5429921
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: McCue, Ann
: APPLICANT: Feldman, Daniel
: TITLE OF INVENTION: Human Calcium Channel Compositions and
: TITLE OF INVENTION: Methods
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Fitch, Even, Tabin & Flannery
: STREET: 135 S. LaSalle
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/745,206A
: FILING DATE: 19910815
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Feder, Scott B
: REFERENCE/DOCKET NUMBER: 51504
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-372-7842
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3566 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3273
: US-07-745-206A-24

Query Match 3.5%; Score 130.6; DB 1; Length 3566;
Best Local Similarity 46.4%; Pred. No. 7.2e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
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RESULT 2
US-08-311-363-24
Sequence 24, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Williams, Steven
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 3566 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie, L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SRO ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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ANTI-SENSE: NO
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FEATURE:
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OTHER INFORMATION: Standard name "alpha2e"
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LOCATION: 3290...3579
OTHER INFORMATION:
US-08-455-543A-36

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QY 1108 actcaaggagcatctgcaacaacttctgccaagaagaatggaatgttgatatgctc 1167
DB 984 TGTGGAAGAGCGCGGTGAATATATACAGCCAAAGAAATTTACAGATTATTAAGAGGCT 1043
QY 1168 tgaatgagccttcaacatctgagtgatltcaaccacaacggaacaagaatgta 1227
DB 1044 TTACTTTTGGTTTGAACAGCTGCTTAATATATATGTTTCCAGAGCA-----AATCGCA 1097
QY 1228 gtcaagcattcatatgctataacttgaatgggcgtgtgacaacctatgatacaacttgc 1287
DB 1098 ATTAAGATTATTTATGCTATTTACGAGATGAGAGAGAGAGCCACAGAGATATTTAA 1157
QY 1288 aatacaatgcccagtcgaagaagctgcatctcacaatacctcatccttgagcaggaagcgt 1347
DB 1158 AATACAAAT---AAAGATAAAAAAGTACGTGATTTCAAGTTTTCAGTTGTCACACAAAT 1214
QY 1348 cgttcgagaacaacttaagtgatgctgctgtgccaacaagaatlttaccagaatc 1407
DB 1215 ATGAGAGAGACCTATATACATGATGATGCGTGTGAACCAAGGTTATTTATTAAGAAAT 1274
QY 1408 ccaacttggctgtatgtgcagaagaatgtcatgtaataccttcaacgtygttaagccgcca 1467
DB 1275 CTTCCATTGTTGCAATAAAGAAATCAATCAAGAAATATTTGGATGTTTGGAAAGACAA 1334
QY 1468 aagtcac-----cgacagagagcagatgtgtgtgagcaggaagccttaacttgaaagca 1521
DB 1335 TGGTTTACGAGAGACAAAGCTAAGCAAGTCCAAATGGAATGTTACTTGGAATGCAT 1394
QY 1522 ctctgactgatagtacagggcccgctcctgtatgcaacactgtaagcagatgcgtgttagta 1581
DB 1395 TGGAACTGGGACTTGTTCATTAATGGAACCTTCGCGGCTTCAACCAATACCGGCAATTTG 1454
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DB 1515 TGGAAATATTTAAAGACTGACACGCTTTTACACTGTGCCCCAATGGGTATTAATTAAT 1574

QY 1702 caatcacaaataatgrratatctcgtcgcagcctcgcagcctcgtctgttaagaagaag 1761
 Db 1575 CAATCGATCCTTAATGTTATGTTTATTACATCCAAATCTTCACCAAGAACCCTCAAT 1634
 QY 1762 gaaaaaagcga 1772
 Db 1635 CTCAGGAGCCA 1645

RESULT 4
 US-08-193-078B-25
 ; Sequence 25, Application US/08193078B
 ; Patent No. 5846757
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
 ; STREET: 1660 UNION STREET
 ; CITY: SAN DIEGO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/193, 078B
 ; FILING DATE: 07-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/868,354
 ; FILING DATE: 10-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-53607
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3579 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 35..3289
 ; OTHER INFORMATION: /standard_name= "Alpha-2e"
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..34
 ; FEATURE:
 ; NAME/KEY: 3'UTR
 ; LOCATION: 3289..3579
 ; US-08-193-078B-25

Query Match 3.5%; Score 130.6; DB 2; Length 3579;
 Best Local Similarity 46.4%; Pred. No. 7.3e-22;
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 agaaatacaaaagatgagagaagacgttgcataagaagaattgattgacctccaaactg 405
 Db 210 ATATTATTAGAAATATCAAGATTGTTGTAATGTTGGAACCAATATATGACGACGCTGG 269
 QY 406 taaagaagctgycaaaagaacatggaagagatgtttcaacaagaagctggaagcgtcaagc 465
 Db 270 TAGAAATTTGCAGCCAGGATTTTGAGAAACTTTCAGACCAACGATCTTAACCCCTGGTGA 329
 QY 466 gtctg-----gtggaagctgcagaagaagacacacctgaacatgaatttgatcag 516
 Db 330 GCGTGGCATTGGAGACGGAGAACTTTCAGACGCTCCACAGTGACAGAGAAATTTTGCA 389
 QY 517 actacagatgaatactcaatgctgtgcgataaagtgaaggaaggaagcaggaatt 576
 Db 390 GCATGGAAGTGTCTACTACAAATGCAAAAGATGATTCGATCCGAGAAATGACAGTG 449
 QY 577 ttltgagctgycgaagaagaaatcattagccccaatgaccatttaataattgcctg 636
 Db 450 AGCCAGGACGCCAGAGATTAACCTGTTTCATTGGAAGATCTAATTTTGACAGACAAA 509
 QY 637 tgaacatcagctcgaagtcgaagtcacaaagaacatgtacaaagaacccctgcaa 696
 Db 510 TATCTTATCAGCAGCAGCAGCAGTCCATATCTCTACTGACATCTATGAGGGCTCAACAAATTG 569
 QY 697 ttgtcaatgaggttattatgctcgaatcctcaacaagaatttltgataacttggacc 756
 Db 570 TGTTAATGAACTCAACTGAGCAGCAAGTGCCTTAGATGAATTTTCAAAAAGAAATGGCAGG 629
 QY 757 gtgaccatctcctcatatgycagtaacttltgaaagtcgaagagccttlttgagcagatc 816
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 QY 817 cgggagatlaaagtggaaccagatgagaatggaagtcattgacctgac-----tgca 867
 Db 690 CAGCTTCACCATGGGTTGATATATGAACTCCAAATTAAGATTGACCTTTATGATGTAC 749
 QY 868 ggaaccgaaaatggtacacccagcagcgaactctccgaagaagcgttggatcattgag 927
 Db 750 GCAGAAGACGATGTGTACATCCAAAGAGGTCGATCTCTTAAGACATGTTATTTGTGGTGG 809
 QY 928 acgtcagtgycagcatgaaaggaactcgtctgactatcgcgaagaacagtcctcatca 987
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 QY 1048 actatgtgaaaccttgcctgcatgaaacttltgtgcgaagccgacaaggaagaagaagc 1107
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 QY 1108 acttcaggagacatcgtgacaacacttgcgcaagaagaattggaatglttgatagctc 1167
 Db 984 TGTGAAAGACGCGGTGATATATATCAACGCCAAAGAAATTCAGATATATGAAGGCGCT 1043
 QY 1168 tgaatgagccttcaaaccttctgagtgatgttcaacacacacagcgaagaagatctgcga 1227
 Db 1044 TTAGTTTGTCTTGAACAGCTGCTTAATTAATTAATGTTTCCAGAGCA-----AAGTGA 1097
 QY 1228 gtccagccatcatgctcataactgagtgagcgtgcgaacctatgatacattcttgcaa 1287
 Db 1098 ATAGATTAATTAATGCTATTCAGCGATGAGAGAGAGAGAGCCAGAGATATTAAACA 1157
 QY 1288 aatacaatlgccagatcgaagaagtltcgacatctcaacatcattatggacgaagcgtg 1347
 Db 1158 AATACAAAT--AAAGATAAAAGTAAGTACGTGATTCAGGTTTTCAGGTGCTCAACAAATT 1214
 QY 1348 cgttgcgaacatcctaaagtgtgagcctgtgcacaacaagatltttaccagatct 1407

Db 1215 ATGAGAGAGACCTATTCAGTGGATGGCCGTGTAACAAAGGTTATTATTAATGAATTC 1274
Qy 1408 ccaccttgctgcatgctgcagagagatcgcagatacccttcgctgtagccggccca 1467
Db 1275 CTTCCATTGGTGCATTAAGATCAATACACAGATATTGGATGTTTGGAGAACCA 1334
Qy 1468 aagtcac-----cgaccggagacatgctgctgctgagcgaagcttacatgcagca 1521
Db 1335 TGGTTTACAGAGCAACAAAGCTAACAGTCCAAATGACAAATGTTACTGGATGCAT 1394
Qy 1522 cctcgtcgtatgctcagggcccgctcctcgtatgcacactgtaagccatgcctgctttagta 1581
Db 1395 TGGAACTGGACTTGTTCATTTACTGGAACCTCTCCGCTTTCAACATPAACGGCCAAATTG 1454
Qy 1582 agcagaacgaacacagatcgcagagagcatctctcctgagagtgctgcacagctccag 1441
Db 1455 AAAATTAAGACAACTTAAGAACACCACTGATTTTGGTGTGATGGAGTAGATGTCTT 1514
Qy 1642 tgaagaactctgaaagacacccccaataacaaagtlaggaatcaggtatgctcttg 1701
Db 1515 TGGAAATATTAATAAGACTGACACAGCTTTTACACTGTGCCCAATGGGTTACTTTG 1574
Qy 1702 caatcacaataatgtrtatctcctgacgcatcgcgaactcaagctgctgtaagaaga 1761
Db 1575 CATTCGATCCTATATGGTTATGTTTATTAATCAATCAATCTTACGCAAAAGAACCCCAAT 1634
Qy 1762 gaataaagcga 1772
Db 1635 CTCAGAGGCCA 1645

RESULT 5
US-08-223-305C-36
Sequence 36, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McGue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/603,751
;; FILING DATE: 04-APR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US89/01408
;; FILING DATE: 04-APR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/176,899
;; FILING DATE: 04-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 52516 (P519739)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619)238-0999
;; TELEFAX: (619)238-0062
;; INFORMATION FOR SEQ. ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3579 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 35..3289
;; OTHER INFORMATION: Standard name "alpha2"
;; NAME/KEY: 5' UTR
;; LOCATION: 1..34
;; OTHER INFORMATION:
;; NAME/KEY: 3' UTR
;; LOCATION: 3290..3579
;; OTHER INFORMATION:
;; US-08-223-305C-36

Query Match 3.5%; Score 130.6; DB 2; Length 3579;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
Qy 346 agaatatacaaaagatctgaaagacgttcacataagaagaatctgctcccaactg 405
Db 210 ATATTATGAGAAATATCAAGATTGTATACGTGGAACCAATATATGACGCCACCTGG 269
Qy 406 taaagaagcttgcaagaacatgaaagagatgtttcacagaagaagcttgaggccgtcagc 465
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Qy 466 gtctg-----gtggaaggctgcagaagaagcacacacctgaaacatgaaattgagcag 516
Db 330 GCCTGGCATTTGGAAGCGGAGAAAGTTCAAGCACCTCACCAGTGGAGAGAAAGATTGGCA 389
Qy 517 acttacagatataacttaactcctgctgctgctgataaaatgaaagagcaaaagcgggaatt 576
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Db 510 TATCTTATGACGACGACGAGATGTCATATTCCTACTGACATCTATGAGGCTCAACCAATTG 569
Qy 697 ttgtcaatggggtttatgtctgaaatcctaaacaagaattttgtagaatacttgacc 756
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Db 810 ATGTGAGTGAAGGTGATGAGGATTTGACACTTAACGTGATCCGAACTCTCTCCGAA 869
QY 988 ttctgatacactgggagatgactctctcaacataatgcttaataatgagagcttc 1047
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QY 1048 actatgtggaaccttgccctgaaatggaacttggtgcaagccgacagacaaagaagc 1107
Db 930 AGAGTGAAGCTGTTTCCACACC-----TTGTCCAAAGCAAAATGTAAGAAATAAAAAG 983
QY 1108 actcagggagcatctgacaacactcttcgcaaggaattggaatggtgataagctc 1167
Db 984 TGTTGAAAGACCGCGTAAATATATATCAGCCAAAGCAATTAAGATATTAAGAGGCT 1043
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QY 1228 gtcaagccatcatgctataactgatactgagtcggtggaacctataacatcttgcaa 1287
Db 1098 ATAGATTTATATGCTATTCAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157
QY 1288 aatacaatlgcagcagcaagtgctcactctcacatccatcactcaggaagagctg 1347
Db 1158 AATACAT-----AAAGTAAAAAAAGTACGTGATTCAGGTTTTCAGTTGCTCAACACAT 1214
QY 1348 cgttcagagaacataaagtgagtgagtcgctgcccacaaagaatcttctaccagatct 1407
Db 1215 ATGAGACAGGACCTATTCAGTGGATGCGCTGTAACAAAGGTTATATATGAAATTC 1274
QY 1408 ccaacttgctgctgctgctgagagagatgctatgataactcactcagctcctagccgcca 1467
Db 1275 CTTCATTTGCTGCAATTAAGATCAATCTCAGGAATATTTGGATGTTGGGAAGACCA 1334
QY 1468 aagtcac-----cgaccagagagcatgctggtgagcaggaagcttaccatgacagca 1521
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QY 1762 gaaaaaagcga 1772
Db 1635 CTCAGGAGCA 1645

RESULT 6

US-08-949-386-32
: Sequence 32. Application US/08949386
: Patent No. 6090623
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Mcclue, Ann
: APPLICANT: Gillespie, Allison
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: US
: ZIP: 92101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/949,386
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/290,012
: FILING DATE: 11-AUG-1994
: APPLICATION NUMBER: 08/149,097
: FILING DATE: 5-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/105,536
: FILING DATE: 11-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 519808
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 238-0999
: TELEFAX: (619) 238-0062
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 35..3289
: OTHER INFORMATION: /standard_name="Alpha-2e"
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..34
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 3289..3579
: US-08-949-386-32

Query Match 3.5%; Score 130.6; DB 3; Length 3579;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
QY 346 agaatcaaaagatgagaagagctgcccataagaagaatgatgagctccaatg 405
Db 210 ATATTATGAGAAATATCAAGATTTGATATGATGAGAACTAAATATATGACAGCGCTGG 269
QY 406 taaagaagctggcaagaacatggaagatgcttcacaaagaagctcgaagcgtcaggc 465

Db 270 TAGAATTGACGAGGATATTGAGAACTTCTGACCAACAGATTCTAAAGCCCTGGTGA 329
Qy 466 gtcg-----gtgaggtctgcagaagacacacctgaaatctgagtcag 516
Db 330 GCGTGGCATTTGGAAGCGGAGAAAGTTTCAGACAGCTCAGCTGAGGAGAAATTTTCCAA 389
Qy 517 actacagatctgaactctgaatctgtctgataaactgaagggaacaaagcgagatc 576
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Db 450 AGCAGGACGACGACGAGATTAACCTGTTTCAATTGAAGATGCAATTTTGGACGACAAA 509
Qy 637 tgaacatcagtcctaaatgagctccaaatgacaaagacatgtaacaaagacccctgaa 696
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Qy 817 cggggaatcaatggaacacagatgaaatgagatcattgctctgac-----tgca 867
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Db 930 AGCATGTAACTGTTTTCAGACACC-----TGTCCAGCAAAATGTAAGAAATTAAGAG 963
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Qy 1522 ctctgactgatacagggcccgctctgataagcactgtagcaatgctglttagta 1581
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Qy 1702 caatcaacaaatgattatatactctgacgacatccgaactcaggctgctgtaacgaag 1761
Db 1575 CAATCGATCCCTAATGCTTATGTTTATTAATCAATCAATCTTCAAGCCAAAGACCCCAAT 1634
Qy 1762 gaaaaagcga 1772
Db 1635 CTCAGAGCCA 1645

RESULT 7
US-08-450-562-32
Sequence 32, Application US/08450562
Patent No. 6096514
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Allison
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/356,257
FILING DATE: 7-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: 08/149,097
3  FILING DATE: 5-NOV-1993
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: 08/105,536
6  FILING DATE: 11-AUG-1993
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: 07/914,231
9  FILING DATE: 13-JULY-1992
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 07/868,354
12 FILING DATE: 10-APR-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: PCT/US92/06903
15 FILING DATE: 14-AUG-1992
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 07/745,206
18 FILING DATE: 15-AUG-1991
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 07/620,250
21 FILING DATE: 30-NOV-1990
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 07/603,751
24 FILING DATE: 08-NOV-1990
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/482,384
27 FILING DATE: 02-FEB-1990
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PCT/US89/01408
30 FILING DATE: 04-APR-1989
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 07/176,899
33 FILING DATE: 04-APR-1988
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Seidman, Stephanie L.
36 REGISTRATION NUMBER: 33,779
37 REFERENCE/DOCKET NUMBER: 6362-519812
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (619) 238-0999
40 TELEFAX: (619) 238-0062
41 INFORMATION FOR SEQ ID NO: 32:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 3579 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: double
46 TOPOLOGY: linear
47 MOLECULE TYPE: DNA (genomic)
48 FEATURE:
49 NAME/KEY: CDS
50 LOCATION: 35..3289
51 OTHER INFORMATION: /standard_name="Alpha-2e"
52 FEATURE:
53 NAME/KEY: 5'UTR
54 LOCATION: 1..34
55 FEATURE:
56 NAME/KEY: 3'UTR
57 LOCATION: 3289..3579
58 US-08-450-562-32
59
60 Query Match 3.5%, Score 130.6; DB 3; Length 3579;
61 Best Local Similarity 46.4%; Pred. No. 7.3e-22;
62 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps
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64 Oy 346 agaattacaagaagatgagaaagacgttgcacatagaagaattatgctgcacactgg 405
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66 Db 210 AATTATTATGAGAAATATCAAGATTTGTACTGTGTGAACCAATATTAAGCACGCGCTGG 269
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70 Db 270 TAGAAATTGCGACCGCGGATATTGAGAAACTTCTGAGCAACAGATCCTAAAGCCCTGGTGA 329
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Qy 1582 AGCAGAGCAAGAACCCAGATCGAAGGCACTCTCTCGGAGTGGTGGCAGAGATGCCAG 1641
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RESULT 8
US-08-984-709A-32
; Sequence 32, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McCauliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..3289
; OTHER INFORMATION: /standard_name="Alpha-2e"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 3289..3579
US-08-984-709A-32

Query Match 3.5%; Score 130.6; DB 4; Length 3579;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
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Db 210 ATATTTATGAGAAATATCAAGATTTTGTATCTGTGACCAATATATGACCGCACTGG 269
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Qy 517 acttaagatgaatcctcaatgctgctgctgataaagaagaagcgaggaatc 576
Db 390 GCATGAGCTTGTCTACTACAAATGCAAGAGATGATCTCATCTGCAAAATATGACAGTG 449
Qy 577 ttltgagctgggaaagaaatcattcagcccaatgacatlttaataattgctg 636
Db 450 AGCGAGGACGACGAGAGATTAACCTGTTTCAATTGACATGCTAATTTGGACGACAA 509
Qy 637 tgaacatcagctaaagtcagtcacgaagtaaccaagacatgtaacaagaacctgca 696
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Db 1215 ATGAGAGAGACCTATTCAGTGTGATGCGCCGTAAACAAAGTTATATATGAATTC 1274
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Qy 1702 caatcaacaataatgtrtatatctgacgcatccggaactcagcgtgctgaagaag 1761
Db 1575 CATTCATCTCTATGCTTATGTTTATTATCATCCAAATCTTCAGCCCAAGAACCCCAAT 1634
Qy 1762 gaaaaaagcga 1772
Db 1635 CTCAGAGCCA 1645

RESULT 9
US-08-455-543A-11
Sequence 11, Application US/08455543A
Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SRO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-455-543A-11

Query Match 3.58; Score 130.6; DB 1; Length 3600;
Best Local Similarity 46.48; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

Qy 346 agaatacaagatagagaagaagcgttgcataagagaatgtatggtcctcaactgg 405
Db 210 ATATTATGAGAAATATCAAGATTGTATCTGTGAACCAATTAATCCACGCCAGCTGG 269
Qy 406 taagaagctgcaagaacatggaagatgcttcaacaagaagctgagccgtcagc 465
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Qy 466 gtctg-----gtgagcgtcgagaagaagcacaccctgaaacatgaattgatgag 516
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Qy 517 actaagtagaatacttcaatgctgctgataaatagaaggagacaagaagggat 576
Db 390 GCAATGAAGTTGCTACTACATCAATGCAAGATGATCTGATCTGAGAAATATGACAGTG 449
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Qy 697 ttgtcaatggggtttatgtgtcgtgaatcttaacaagaagtttgtgataacttgacc 756
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Db 1635 CTCAGAGACCA 1645

RESULT 10
US-08-455-543A-33

Sequence 33, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: //standard_name= "Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:

NAME/KEY: 3/UTR
LOCATION: 3308..3600
US-08-455-543A-33

Query Match 3.5%; Score 130.6; DB 1; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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DB 330 GCCTGGCATTTGGAAGCGGAGAAAGTTCCAGCAGCTCCACAGTGAGAGAAATTTTGCAA 389
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QY 697 ttgtcaatgaggttattggtctgaatctctaaacaaagttttgtagataacttgacc 756
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DB 870 TGTTAGAAACCTCTCAGATGATGATTTGCTGAATGATGATTTTCAACAGCAATGCTC 929
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DB 1158 AATACAT---AAGATATAAAAGTACGTGATTTACAGTTTTCAGTGTGCTAACACATTT 1214
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DB 1635 CTCAGAGCCA 1645
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RESULT 11
US-08-193-078B-11
Sequence 11, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991

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ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-193-078B-11
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Query Match 3.5%; Score 130.6; DB 2; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
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DB 330 GCCTGGCATTGGAGGCGAGAAAGTTCAAGCAGCTCACCAGTGAAGAGAAATTTTGGCAA 389
QY 517 acctacagatagaataactccaatgcctgctgataaaagaagaagacgaagcgggaatt 576
DB 390 GCAATGCAACTGTCTACTCAATGCAAGAGATGATCTCATCTCTGAGAAAAATGACAGTG 449
QY 577 tcttgagagctgggaagaatcatccttagcccaaatgacatttaatttgacctg 636
DB 450 AGCCAGGCGCAGAGGATAAACCTGTTTCAATTGAGATGCTAATTTTGGACGACAAA 509
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DB 510 TATCTTATCAGCAGCAGGAGCTCAATATCTACTGACATCTATGAGGGCTCAACAATTG 569
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DB 630 AAGACCCCTTCAATTATTTGGCAGGTTTTTGGCAGTGCCACTGCGCTGATATTTATC 689
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DB 870 TGTAGAAACCCCTCAGATGATGATTTTCTGATGATGATTTTAAACGCAATGCTC 929
QY 1048 actatgtgaacacttgctgaatgaaacttggctgaagcgcgaagcaacaagaagc 1107
DB 930 AGGATGTAAGCTGTTTTCACACC-----TTGTCCAGCAAAATGTAAGAAATAAAG 983
QY 1108 acttcaggagatcttggaacaaacttctgcgaagaagaattgaaatgctgatatgctc 1167
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QY 1168 tgaatgagcctcaacatctgagtgatctcaaccaacagggacagaagatctgca 1227
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DB 1215 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1274
QY 1408 caaccttgctgctgctgctgaggaatgctgaataacatcttcaacgtctgacggccca 1467
DB 1275 CTTCATTTGCTGCAATTAAGATCAATCAACGAGAAATTTGATGTTTGGAGAACAA 1334
QY 1468 aagtcac-----cgaacgaagcagatgagtgctgagcagagatctcatgtgaagca 1521
DB 1335 TGTGTTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394
QY 1522 cctcgtactgatatgctcagggcccccgtcctgtagcaacatgtagcagctgctgttagta 1581
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DB 1455 AAAATTAAGCAAACTTAAGAACACACACTGATTTCTGTTGATGAGGAGATGATGCTCT 1514
QY 1642 tgaagaacacttgcgaagacatcccaataacagttgaatgctcaggtttagccttg 1701
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QY 1702 caatcaataatgtrlatatcctgaacatccggaactcaagctgctgtaagaag 1761
DB 1575 CAATGATCTCTAATGTTATGTTTATTAATCAATCAATCTTCAAGCAAAAGAACCCCAAT 1634
QY 1762 gaaaaagcga 1772
DB 1635 CTCAGAGAGCA 1645
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RESUME 12
US-08-223-305C-11
Sequence 11, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
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QY 1522 cctctactgataatcagggcccccctcctgatacaccctgtaacatgacctgtttagta 1581
DB 1395 TCGAAGTGGAGCTTGTCAATTAAGTCTTCCGGTCTTCAACATTAACCGGCAATTTG 1454
QY 1582 agcgaagacaaacccgatacgcagggcattcctcctggaagtgtgtgcacagatgtccag 1641
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DB 1515 TCGAAGATTTAAAGACGACACCGCTTTTACACTGTGCCCAATGGGATTAATTTG 1574
QY 1702 caatcaaaataatgrrtataatcctgacgcagcactcagcgtcgtacgaagaag 1761
DB 1575 CAATGATCTTAATGTTATGTTTATATCAATCAAAATCTTCAGCCAAAGAACCCCAAT 1634
QY 1762 gaaaaaagcga 1772
DB 1635 CTCAGCAGCCA 1645

RESULT 13

US-08-223-305C-33

Sequence 33, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223, 305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868, 354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745, 206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620, 250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482, 384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603, 751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176, 899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-223-305C-33

Query Match

3.5%; Score 130.6; DB 2; Length 3600;

Best Local Similarity 46.4%; Pred. No. 7.3e-22;

Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 agaaatcacaaagatgatgaagaagcgttgcatagaagaatltgtagcctccactg 405
DB 210 ATATTATGAGAAATCAAGATTTGTATCTGTGGAACCAATATATGACCGCAGCTGG 269
QY 406 taagaagctgcgaagaacatggaagatgtttccaaagaagctgagccgctcagc 465
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DB 390 GCAATGAACTGTCTACTCAATGCAAGATGATCTCGATCGAAGAAATGACAGTG 449
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DB 570 TGTAAATGAACCTCAACTGAGACAGTGCCTTAGATGAATTTTCAAAAAGAAATCCGAGG 629
QY 757 gtgaccatctcatalagcagtaactttggaagtgcaagagccttlttgaagatgc 816
DB 630 AAGACCCCTTCATTATTGTGGCAGGTTTGGCAGTGCCACTGACCTGATATTATTC 689
QY 817 cggggaaltaaatggaacagatgaagaatgagatcattgaccttcgac-----tgca 867
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QY 868 ggaacgaaatgtgtacatcagcagcaactctcgaagaagcgtggtcatttgaattg 927
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DB 810 ATGTAGTGAAGTGTAGTGTGATTGACACTTAACCTGATCCGAACATCTGTCCGAAA 869


```

1 ADDRESS: Brown, Martin, Haller & McClain
2 STREET: 1660 Union Street
3 CITY: San Diego
4 STATE: California
5 COUNTRY: USA
6 ZIP: 92101-2926
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patentin Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/149, 097D
15 FILING DATE: 05-NOV-1993
16
17 CLASSIFICATION: 435
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/105,536
21 FILING DATE: 11-AUG-1993
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: WO PCT/US92/06903
25 FILING DATE: 14-AUG-1992
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/914,231
29 FILING DATE: 13-JUL-1992
30
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/868,354
33 FILING DATE: 10-APR-1992
34
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 07/745,206
37 FILING DATE: 15-AUG-1991
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39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/620,250
41 FILING DATE: 30-NOV-1990
42
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 07/482,384
45 FILING DATE: 20-FEB-1990
46
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: US 07/603,751
49 FILING DATE: 04-APR-1989
50
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: WO PCT/US89/01408
53 FILING DATE: 04-APR-1989
54
55 PRIOR APPLICATION DATA:
56 APPLICATION NUMBER: US 07/176,899
57 FILING DATE: 04-APR-1988
58
59 ATTORNEY/AGENT INFORMATION:
60 NAME: Seidman, Stephanie L.
61 REGISTRATION NUMBER: 33,779
62 REFERENCE/DOCKET NUMBER: 6362-55038
63 TELECOMMUNICATION INFORMATION:
64 TELEPHONE: (619) 238-0999
65 TELEFAX: (619) 238-0062
66
67 INFORMATION FOR SEQ ID NO: 11:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 3600 base pairs
70 TYPE: nucleic acid
71 STRANDEDNESS: double
72 TOPOLOGY: linear
73
74 MOLECULE TYPE: DNA (genomic)
75
76 FEATURE:
77 NAME/KEY: CDS
78 LOCATION: 35..3310
79 OTHER INFORMATION: /standard_name="Alpha-2"
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81 FEATURE:
82 NAME/KEY: 5'UTR
83 LOCATION: 1..34
84
85 FEATURE:
86 NAME/KEY: 3'UTR
87 LOCATION: 3308..3600
88
89 US-08-149-097D-11

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Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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Oy 406 taagaagctggcaaaagaacatgaaagatglttcacaagaagctcgagccgtcagcg 465
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Db 270 TGAATATTCAGCAGCAGGATATTGAGAACTTCTGAGCAACAGATCTTAAAGCCCTGGTGA 339
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Oy 466 gctcg-----gtggagctcgcaagaagcacactgaaacatgaaatttgatcgag 516
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Db 330 GCCTGCATTTGAAAGCGGAAAGTTTCAAGACCTCACCAAGTGGAGAAATTTTGCA 389
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Oy 517 acttaacagatgaatacctcaatctgctgctgataaagaagaagcaagagcggaatt 576
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Db 390 GCAATGAGATTTGTCTACTCAATGCAAGAGATGATCTCGATCTGGAAATAATGACAGTG 449
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RESULT 15
US-08-949-386-11
Sequence 11, Application US/08949386
Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McGue, Ann
APPLICANT: Gillespie, Alison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: (619) 238-0999
; TELEFAX: (619) 238-0062
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3600 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 35..3310
;   OTHER INFORMATION: /standard_name="Alpha-2"
; FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..34
; FEATURE:
;   NAME/KEY: 3'UTR
;   LOCATION: 3308..3600
; US-08-949-386-11

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Query Match      3.5%; Score 130.6; DB 3; Length 3600;
Best Local Similarity 46.4%; Pred. No. 7.3e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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Db 1635 CTCAGAGGCCA 1645

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Search completed: August 16, 2002, 20:11:22
Job time: 14332 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 16:02:20 ; Search time 3811.76 Seconds

(without alignments)
13349.088 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770

Sequence: 1 tactatagggcgcgcgcga.....aaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gD_estl:*
10: gD_estl2:*
11: gD_hic:*
12: gD_gss:*
13: em_gss_hum:*
14: em_gss_inu:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	784.8	20.8	880	10	BT515864 603184526
3	784.2	20.8	798	10	BT206136 RST25571
4	688.8	18.3	738	9	AV723130
5	647.2	17.2	818	10	BE740459
6	633.4	16.8	801	10	BT213431
7	583.8	15.5	608	9	AV722352
8	561.2	14.9	762	10	BT218214
9	518.4	13.8	799	10	BT736456
10	515	13.7	671	10	BE985092
11	492.4	13.1	711	10	BT736450
12	479.4	12.7	589	10	BT465072
13	458	12.1	505	10	BT924114
14	448.8	11.9	570	9	BT928328
15	447.2	11.9	570	9	BT929346
16	432.4	11.5	843	10	BT732344
17	432.2	11.5	782	10	BT295845

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19	420	11.1	420	9	AI880300
20	419	11.1	422	9	AI88635
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22	405.2	10.7	551	9	AM655372
23	404.4	10.7	502	9	AM491939
24	401.4	10.6	450	9	AI290166
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39	330.6	8.8	428	9	AA815447
40	328.8	8.7	332	10	BE768727
41	328.2	8.7	365	10	BE764499
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ALIGNMENTS

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BT53834 603027515F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5198019 5',
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 966)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1AM1495 row: n column: 04
High quality sequence stop: 784.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:5198019"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ. brain. Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."

BASE COUNT 258 a 221 c 234 g 251 t 2 others

ORIGIN

Query Match 21.6%; Score 813; DB 10; Length 966;
Best Local Similarity 94.3%; Pred. No. 1.6e-108;
Matches 919; Conservative 0; Mismatches 47; Indels 9; Gaps 7;

QY 2526 agtaccatccatccagctccttgatgaaaggaacccctcgtggtgagcagctgtaggcatt 2585
|||||
DB 1 agtaccatccatccagctccttgatgaaaggaacccctcgtggtgagcagctgtaggcatt 60
|||||

QY 2586 cagatgaacttgaacttttccaaaggaagcttcgtgacctgacagcagcagctgtgcttc 2645
|||||
DB 61 cagatgaacttgaacttttccaaaggaagcttcgtgacctgacagcagcagctgtgcttc 120
|||||

QY 2646 ctgagatgcaaaatgctcctcctgagcagctgagcagctgagcagctgagcagcagcagc 2705
|||||
DB 121 ctgagatgcaaaatgctcctcctgagcagctgagcagctgagcagctgagcagcagcagc 180
|||||

QY 2706 aatgaaggttcttcttctgctgagcagcagcagcagcagcagcagcagcagcagcagc 2765
|||||
DB 181 aatgaaggttcttcttctgctgagcagcagcagcagcagcagcagcagcagcagcagc 240
|||||

QY 2766 atcgaagagctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2825
|||||
DB 241 atcgaagagctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
|||||

QY 2826 tatgactacaaagcagctgctgagcagcagcagcagcagcagcagcagcagcagcagc 2885
|||||
DB 301 tatgactacaaagcagctgctgagcagcagcagcagcagcagcagcagcagcagcagc 360
|||||

QY 2886 ctgagatccctataagcctcctcctcctgagcagcagcagcagcagcagcagcagcagc 2945
|||||
DB 361 ctgagatccctataagcctcctcctcctgagcagcagcagcagcagcagcagcagcagc 420
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QY 2946 ttcctggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3005
|||||
DB 421 ttcctggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 480
|||||

QY 3006 aatctgaaacagacccctgagcagcctgagcagcagcagcagcagcagcagcagcagc 3065
|||||
DB 481 aatctgaaacagacccctgagcagcctgagcagcagcagcagcagcagcagcagcagc 540
|||||

QY 3066 accatcaaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3125
|||||
DB 541 accatcaaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 599
|||||

QY 3126 cagcaaatcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3185
|||||
DB 600 cagcaaatcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 659
|||||

QY 3186 tctgtgcccac 3245
|||||
DB 650 tctgtgcccac 719
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QY 3246 gaaagcttcaaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3305
|||||
DB 720 gaaagcttcaaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 776
|||||

QY 3306 gaggagaatgcaag 3365
|||||
DB 777 gaggagaatgcaag 835
|||||

QY 3366 ctgtccctcctgcttctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 3425
|||||
DB 836 tctgtccctcctgcttctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 894
|||||

QY 3426 gactgagatgtctctctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 3485
|||||

DB 895 GACTGAATG-TCTCTGGATGGTTAATCATGG--TAACCTGACAAATAATGGGCGAC 951
QY 3486 aacatacagacatg 3500
|||||

DB 952 TACACACTGAATG 966

RESULT 2
BI915864 880 bp mRNA linear EST 16-OCT-2001
LOCUS 603184526F1 NIH-MGC_121 Homo sapiens CDNA clone IMAGE:5248447 5',
DEFINITION mRNA sequence.
ACCESSION BI915864
VERSION BI915864.1 GI:16179807
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 880)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1627 row: c column: 08
High quality sequence stop: 740.
Location/Qualifiers
1..880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5248447"
/clone_1lb="NIH-MGC_121"
/lab_host="PH10B"
/note="Organ: Drains: Vector: pCMV-SPORT6; Site_1: NOTI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH-MGC Library."

BASE COUNT 257 a 221 c 175 g 227 t

ORIGIN

Query Match 20.8%; Score 784.8; DB 10; Length 880;
Best Local Similarity 96.6%; Pred. No. 2e-104;
Matches 823; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

QY 2921 atgagatcatgacagaaactgtctgtctcgtgtggaattaaacttcgcaagttgtgtgca 2980
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DB 1 atgagatcatgacagaaactgtctgtctcgtgtggaattaaacttcgcaagttgtgtgca 60
|||||

QY 2981 ctcgcgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3040
|||||
DB 61 ctcgcgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
|||||

QY 3041 atatcgaagctcgtctcgtgagcgacacacacacacacacacacacacacacacacacac 3100
|||||
DB 121 atatcgaagctcgtctcgtgagcgacacacacacacacacacacacacacacacacacac 180
|||||

QY 3101 agactgctccaagctcttctgcatccagcaaatcccaagcagcagcagcagcagcagcagc 3160
|||||

Db 181 AGACTGCTCCAAAGTCCTTGTGATCCAGCAAAATCCAGACGACACCTGTTGATGNGT 240

Qy 3161 ggttgagcaagcagctgctctgtgaaatctgtgcccccaaccatgga>accattgaat 3220

Db 241 GGTGGACACAGCTGCTGCTGTGAATCTGTGGCCCCCACCATGCAACCATTTGAAAT 300

Qy 3221 caggtaataagatcccttaagtgtgaaagctcaagaagcccaagaatccagaagcgccc 3280

Db 301 CAGGTTAATGAAATCCCTTAAGTGAAGTCAAGCTCAAAAGGCCCAAGACATCGAAGGCGCCC 360

Qy 3281 agaattctgcatggtctccatccctgaggagaatgcaaggaagtgtgagggtgcgcag 3340

Db 361 AGAATCTTGTCAAGCTTCATCCATCCAGAGAAATGCAAGGAGTGTG3GGGTGCGCGAG 420

Qy 3341 tctccaagcccgacagctctctctctgtctccctcgctt-tgatgtctcttcaagt 3399

Db 421 TCTCCAAAGCCCAAGACAGTCTCTCTGCTCCCTGCTTTCGATGATGCTCTTCAAGT 480

Qy 3400 gaacactgagatgttctcttactgactgagatgttctctgtgcatgtcataatcag 3459

Db 481 GACACGATGAGATGTTCTCTTACTGACTGAGATGTTCTTGGCAATGCTTAATCATG 540

Qy 3460 ataaactgtgaacccaataatagtgcaacatacagagacataagataatgccaacacag 3519

Db 541 ATAAACTGTGAACCAAAATATGAGTGCAACATGACGATGATATATATGTCACATCAG 600

Qy 3520 catctcatatgatttaaacgtgtgcatataaacctttaaagatagttgaacaaaa 3579

Db 601 CATCTCATATGATTTTAAACGTGTGATATATTAACCTTTAAAGATATGTTACAAAAA 660

Qy 3580 gtatcatcatcttcttcttcttctgcaagtcagatgaaatgtgaattgtgccaatgaatc 3639

Db 661 GTTATCTATCATCTTTTACTTACAGCAGTCATGCCAATGTGAGTGTGCCACATGATATC 720

Qy 3640 acccttcacagaatagtggaacgcaagtgtga-tgcaagtctccctctgtctgaaccta 3698

Db 721 ACCCTTCATCAGAAATATGGAACGCAAGTGTACAGCAGTGTCCCTTCTGTTGAACCTA 780

Qy 3699 ttgaaacccaatttaaacgtgttactctttaaataagataatataataataaaaaa 3758

Db 781 ATCGAACCAATTTAACAGTGTACTTACTTAACATACGATATATTCACACTCTCATACAC 840

Qy 3759 aaaaaaanaaa 3770

Db 841 AACACCAACAA 852

RESULT 3

LOCUS BG206136 798 bp mRNA linear EST 21-APR-2001

DEFINITION R5725571 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG206136

VERSION BG206136.1 GI:13727823

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 798)

AUTHORS Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cochran,K., Do,K., Offenbacher,J., Danzig,J., and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 21277151

COMMENT Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 551.

Location/Qualifiers

1..798

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="H1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 215 a 196 c 178 g 209 t

ORIGIN

Query Match 20.8%; Score 784.2; DB 10; Length 798;

Best Local Similarity 99.0%; Pred. No. 2.5e-104;

Matches 789; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2822 ccttaatactaccagcaatgtagagccaagaagaacagcagatgagcccatg 2881

Db 1 CCTGTATGACTTACCATGCTCATGTGTAGACCAACAAAGAAAGCAGCATGGCCCATAG 60

Qy 2882 ccttcctgatactataatgctctctctctgcagtaaatgatacagaaacttgt 2941

Db 61 CTTCTTGAGATCTTATATATCTCTCTCCGCGATGAAATGATGATGACAGAACTGT 120

Qy 2942 ctgtctctgtggaatttaacaccttgcaattgtgtgacatccgataatgcaagtaagc 3001

Db 121 CTTGTTCTGCTGGAATTTAACTCTGACATGAGTGAGCAGCTCCATATGACAGCTAAAG 180

Qy 3002 ccagaatctgaacagacccttgagaccttgatatacgaatataccaacatctgtctga 3061

Db 181 CCAGAAATTTGAACAGACCCCTGGAGCCTAGTGAATGATGATGATGATGATGATGAT 240

Qy 3062 gcgcacacatcaagagagatacaggaatattgctgtgaaagactgtccaaagtccttgt 3121

Db 241 GCGCACCATCAAGAGAGCTACAGGAAATATGCTTGAAGACAGCTCCAAAGTCTTTGT 300

Qy 3122 catccagcaaatcccaagcagcaacacctgtcatatggtgtgtgtgagagcagctgctctg 3181

Db 301 CATCCAGCAAAATCCAAAGCAGCAACCTGTTCATGCTGTGAGCAGCAGCTGCTCTG 360

Qy 3182 tgaatctgtgcccccaatcaacatgagcaccatgaaatcagatataatcccttaa 3241

Db 361 TGAATCTGTGGCCCCCATACACATGCGACACCATTTGAATGATGATGATGATGATGAT 420

Qy 3242 gttgaaagcttaagagccagaagatcagaagcgcccaagatctgtcatgtctcca 3301

Db 421 GTGTGAACGTCTAAAGCGCCAGAGATCAGAAGCGCCCGCAAAATCTGTGATGCTTCCA 480

Qy 3302 tccctgaggaatagcagaagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3361

Db 481 TCTCGAGAGAAATCCAAAGGAGTGTGGGGTGGCCCAAGTCTCCAAAGCCCAAGAGTCT 540

Qy 3362 cctctgtccctctctgtcttctgtatgctctctcaaggtgacaactgagatgtctct 3421

Db 541 CTTTCTGCTCCCTCTGTTTGAATGCTCTTCTCAAGGTGACACAGTGAAGATGCTCTCT 600

Qy 3422 taactgactgagatgttctctgtgcatgataatcaatgataaactgtgaacaaatag 3481

Db 601 TACTGACTGAGATGTTCTCTTGGCATCTTAATCATGATGAATGATGATGATGATGATG 660

Qy 3482 gtccaacatcgagacatgataatagtcacaacatcgagatcagatcagatcagatcag 3541

Db 661 GTGCAATATGAGACATGATATAGTCCAAACATTCAGATTCATATGATGATGATGATGAT 720

Qy 3542 gtgcgtgataataacttaagaatagatgttgacaanaagatatacatcatcttact 3601

Db 721 GTGGGTATATAAAGCTTTAAAGATATGTGGACAAAGTTATCTATCATCTTTTACTT 780

OY	3602	tgcacgcatcgtcaaatg 3618
Db	781	tgccagtcattgccaaatg 797
RESULT	4	
LOCUS	AV723130	738 bp mRNA EST 16-OCT-2000
DEFINITION	AV723130 HTB Homo sapiens cDNA clone HTBAPB04 5', mRNA sequence.	
ACCESSION	AV723130	
VERSION	AV723130.1 GI:10826300	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 738)	
AUTHORS	Gu,Y., Peng,X., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu, 'S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,U., Chen,Z. and Han,Z.	
TITLE	Homo sapiens cDNA HTB clones	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel.: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzgeg@chc.sh.cn This clone is available at CHGC in Shanghai.	
FEATURES	Location/Qualifiers	
SOURCE	1..738 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HTBAPB04" /clone_lib="HTB" /tissue_type="Hypothalamus" /dev_stage="adult" /lab_host="SOLR" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT	196 a 182 c 180 g 180 t	
ORIGIN		
Query Match	18.3%; Score 688.8; DB 9; Length 738;	
Best Local Similarity	97.7%; Pred. No. 1.7e-90;	
Matches 721; Conservative	0; Mismatches 12; Indels 5; Gaps 2;	
OY	2072	ggcagatgaatagtgtctctactctgaacacacgtgaccttaacccttagacacgcgcacatctgtctcca 2131
Db	1	ggcacatatgaataggctcttactctgcacacacgtgaccttaacccttagacacgcgcacatctgtctcca 60
OY	2132	gttaagaacggaattaaagcctcaccctaagaaggacaagaacctctgtccagttgatataaga 2191
Db	61	gttaaacacgattaaagctcttactttaaaagcgcaaaagAACACTTGTGTCAGTGATTAAGA 120
OY	2192	attgaatcacaagaagctcctttttgacgcggtggtgagtgcccccatitgaagcgtattggac 2251
Db	121	ATTGATCCAAAGAGTCCTTTTGAACGCCGAGAGGTGAGTAGTCCCCCATTTGAAGCGTATTGGAC 180
OY	2252	cagcctggcctctcaacaataatcttgacacaaggcggtgagaggttgtcctctctcg 2311
Db	181	CAGCCTGGCCCTCAACAATCTGAAAATTCTGACAAAGGCGCTGGAGGTTGGCTTCTCTCGG 240
OY	2312	cactgcacagggcctctctcagaalcaaacctgtttgtcgggctggaagcgcacaccaatca 2371
Db	241	CACGTCCGACGGGGCCCTCTCCAGATCAACCTGTGTTCTCGGGCTAGCAGCTCACCAATCA 300
OY	2372	ggaactctcgaagaagctggcgacaaggagaaacattttaagcagaacaaatttcctctctg 2431

DB	301	GGACTTCTCCGAAGCTGGGACACAGAGACATTTTAAACGACACATTTCCCTCTCG	360
OY	2432	gtaccgaagagccgctgtagcagatccaggagagctcgltcactcgatcccatcagac	2491
DB	361	gtaccgaagagccgctgtagcagatccaggagagctcgltcactcgatcccatcagac	420
OY	2492	tggaccagtcgaataaagaatgtgtgtgacagcaagttcatccatccagctctgtatga	2551
DB	421	tggaccagtcgaataaagaatgtgtgtgacagcaagttcatccatccagctctgtatga	480
OY	2552	acggaaatccctgt	2611
DB	481	acggaaatccctgt	540
OY	2612	gaagttctgtgactgcagacagacagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2671
DB	541	gattgt	600
OY	2672	tgtatgt	2731
DB	601	tgtatgt	659
OY	2732	agaccac	2791
DB	660	agaccac	715
OY	2792	gctaacatgt	2809
DB	716	gctaacatgt	733
RESULT	5		
LOCUS	BE740459	818 bp	mRNA linear EST 15-SEP-2000
DEFINITION	601595508.1 NIH_MGC_9	Homo sapiens	CDNA clone IMAGE:3949657 5',
ACCESSION	BE740459		
VERSION	BE740459.1	GI:10154451	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 818)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: DCTD/DP		
	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLB at: image.lnlb.gov		
	Plate: L1C6M814 row: 0 column: 02		
	High quality sequence stop: 774.		
FEATURES	location/Qualifiers		
SOURCE	1..818		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3949657"		
	/clone_lib="NIH_MGC_9"		
	/tissue_type="adenocarcinoma cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: ovary; Vector: pOTB1; Site_1: XhoI; Site_2:		
	EcoRI; cDNA made by oligo-AT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adapter: GGACGAC(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."		

BASE COUNT 244 a 169 c 205 g 200 t
ORIGIN

Query Match 17.2%; Score 647.2; DB 10; Length 818;
Best Local Similarity 89.4%; Pred. No. 1.8e-84;
Matches 794; Conservative 1; Mismatches 14; Indels 79; Gaps 6;

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QY 954 cgcctgactatcgcggaagcaaacagctcatttctgatacacttggtgatgac 1013
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Db 1 CGCTGACTATCCGGAAGCAACAGCTCATCTTTCATCTTGGATACACTTGGGATGATGAC 60
QY 1014 ttcttaacaataatttcttaataaggaagctcactatgttgaaaccttgcctgaatgga 1073
    |||
Db 61 TTCTTCAACTAATTGCTTATATGAGGACCTTCACTATGTGAACTTGCCTGAATGGA 120
QY 1074 acttctgtgaagcgcagagcaaacaaagaaagcacttcaggaggacacttcgcaaaact 1133
    |||
Db 121 ACTTTGGTGCAGCCGACAGACAAACAAAGACACTTCAGGGAGCATTCGACAAACTT 180
QY 1134 ttgcgcaaaagaaatttggaatgttgatatagctcttgaaagagccttcaactctgaat 1193
    |||
Db 181 TTGCCAAAGGAATGGAAATGGATATAGCTCTGATAGAGGCTTCAACATCTGAGT 240
QY 1194 gattcaacacacagcgagcaagaaagatattctgagtcaggccactgctcactaactgat 1253
    |||
Db 241 GATTTCAACACACAGGACAGAGAAATGTGAGTGAAGCCATCATGCTATTAACGTAT 300
QY 1254 gggcggttgagacacactatgatacaatcttgcacaaataacatctggccagatcgaaagtc 1313
    |||
Db 301 GGGGCGGTGACACACTATGATACATCTTGCACAAATACAAATGGCCAGATCGAAAGTT 360
QY 1314 cgcattctcaacatacctcattatgacgagaggtgcgttgcgcagacaaactcaaatgtgac 1373
    |||
Db 361 CGATCTTTCATACCTCATCTGATGACGAGGCTGCTTCAGACAACTTAAAGTGATG 420
QY 1374 gctctgacacaaagaaatttttcaaccagatctcaaccttgcctgtgtgcagagaat 1433
    |||
Db 421 GCTGTGCGCAACAAAGGATTTTATCCCAATCTCCACCTTGGTGTATGTGACAGAGAAAT 480
QY 1434 gtcaatgaatcaccttcaagctgcttagccggcccaaaagtcacgacccggagcatgac 1493
    |||
Db 481 GTCATGGAATACCTTCACGCTGATTAGCCCG -CCAAAGTCATCGACGAGCATGATGTG 539
QY 1494 gcttgagacagaaagcttaacatgacagcactctgactgataatgaagcccttcctgac 1553
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Db 540 GTCTGAGACCGAACCTTACATTTGACAGCATT----- 569
QY 1554 accacgttagcactgctgtgtttagtaagcagaacacagatcgaaagggcatctt 1613
    |||
Db 570 ----- -AGATCGAAAGGGCATTCCT 587
QY 1614 ctggagagtggttggcacagatgtccagtgaaagaacttcgaagacatcccccaaatlac 1673
    |||
Db 588 CTGGAGTGGTGGACAGATGTTCCAGTGAAGAACTTGAAGAAATCCCAAAATAC 647
QY 1674 aagttgggaattcaaggttatgcttcttgcaatacaataatggtctatctcgtgacat 1733
    |||
Db 648 AATTTAGGGAATTCACGCTTATGCTTTGCAATCAACAATATGATATAT-CTGACCCAT 706
QY 1734 ccggaactcaaggtgctgtgtaagaaagaaagaaagcgaaggaacttaactatagagc 1793
    |||
Db 707 CCGGAATCAAGGCTGCTGTACGAAGAAAGAAAGCGAAGGA--CTAAGTATAGTA-- 762
QY 1794 gttgacctctctgaggttgaggttggaagaccgaatgacgttggtgaa 1841
    |||
Db 763 CGTTGACTCTCTGAGGTGAGTGGAA -AACGAGATGACGTGTCGAA 809
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RESULT 6
BG213431 801 bp mRNA 1: near EST 21-APR-2001
LOCUS BG213431
DEFINITION RS733037 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG213431
VERSION BG213431.1 GI:13735118
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 801)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Io,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE JOURNAL
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 477.
location/Qualifiers

FEATURES

source
1..801
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 221 a 191 c 183 g 205 t 1 others
ORIGIN

Query Match 16.8%; Score 633.4; DB 10; Length 801;
Best Local Similarity 91.3%; Pred. No. 1.8e-82;
Matches 723; Conservative 0; Mismatches 22; Indels 47; Gaps 3;

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QY 2688 aattgttaacctatagacaataatgatttctgtgtcgaagctacacagact 2747
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Db 13 AATTGTACCTCATAGACAAATATGATTTATTTGGTGTGATGAAAGCATACACAGACT 72
QY 2748 ggaagacttttctgtgagatcagagagctgttgtaacaaattgtcacaatgtgctcc 2807
    |||
Db 73 GGACACTTTTGGTGTGATGAGAGAGAGCTGTGTAAGCAAAATGCTTACGATGGGCTCC 132
QY 2808 tttaaaagaattacccttattgactacaaagcactgtgtagagcacaagaagaagcagc 2867
    |||
Db 133 TTTTAAAGAAATTAACCTTTATGACTACCAAGCATGTGTAAAGCAACAAGAAAGCAGC 192
QY 2868 gatvgcgccaatgagcctcctcgtgaccttaataatgctctcctctcgtgaataatgac 2927
    |||
Db 193 GATGGCGCCCATGCGCTCTCTGATCCCTTATATCCCTTCTCTACAGTAAATGGATC 252
QY 2928 atgacagaacttgcctgttctcgttggtgaatttaacctctgcaatttggtgacatccat 2987
    |||
Db 253 ATGACAGAACTTGTCTGTCTGCTGTAATTTAACTCTCAGTGGTGGCTCCGAT 312
QY 2988 atgacagctaaagcccaagaatttgaacagaccccttgagaccttctgatactgaaatca 3047
    |||
Db 313 ATGACAGCTTAAAGCCCAAGAAATTTGAACAGACCCCTTGAGTGAATCAATATACCA 372
QY 3048 gcaatgctctctgagcgacacatacaagagactacaaggaatattgcttgaagactgc 3107
    |||
Db 373 GCATTCGCTCTGAGCGCACCATCAAGAGACTCAAGGAAATATTGCTTGAAGACTGCG 432
QY 3108 tcaagtccttctgcatccagcaaatcccaagcagcaacctgttcatggtgtgtgtgac 3167
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Db	433	TCCAAATCCTTGTGTCATCCAGCAATCCCAACAGCAACCTGTATCGTGGGGTGGAC	492
Qy	3168	agcagctgcctcttgcgaatctgtgtgcccccaaccaatggcaccatctgaatacag----	3223
Db	493	AGCAGCTGCCTGTGGAATCTGTGGCCCCCATCACCATTGGCAACCATTAATAATCAAGTA	552
Qy	3224	-----gataaataaatcccttaagt	3243
Db	553	GAAAAAGCAATCCTTGGAAACATGCCCTTAACCTACAGTCACATATAATGAATCCCTTAAT	612
Qy	3244	gtgaacgccttaagaagcccaagaatcaagaagcgcccaagaatcttgtcaatgcttcacac	3303
Db	613	GTGAACGCTCTAAAGGCCCAAGAAATCAGAAAGCGCCCAAGAGCTCTGTGCTTCCATC	672
Qy	3304	ctgaagagaatcaagaaggagtggtgggggtgcgcgagatctccaagcccaagaagtcctcc	3363
Db	673	CTGAGGAGAAATTCAGAAAGATGTGGGGGTGCCCCCAAGTCTCCAAAGCCCAACAAAGTC--CC	730
Qy	3364	ctctgcctccctctgccttttgatgctctcttcacaagltgaacactgaactgaatgtttctcta	3423
Db	731	CTCTTTCCTCCTCTCTTTTGAATGATGCTTCTC--AGGGAGACATGACATGATGTCTTTTA	789
Qy	3424	ctgaactgaatg	3435
Db	790	CTGACTGAATG	801

RESULT	7
AV722352	
LOCUS	AV722352 608 bp mRNA linear EST 16-OCT-2000
DEFINITION	AV722352 HTB Homo sapiens cDNA clone HTBAVB10 5', mRNA sequence.
ACCESSION	AV722352
VERSION	AV722352.1 GI:10824752
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 608)
AUTHORS	Gu,Y.,Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,,

TITLE	Homo sapiens CDNA HTB clones
JOURNAL	Unpublished (2000)
COMMENT	Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES	Location/Qualifiers
source	1. .608

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTBAVB10"
/clone_1lb="HTB"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2
XhoI"
BASE COUNT      159 a      150 c      141 g      157 t      1 others
ORIGIN

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Query Match	15.5%;	Score 583.8;	DB 9;	Length 608;
Best Local Similarity	98.8%;	Pred. No. 2.8e-75;		
Matches 599; Conservative	0;	Mismatches 3;	Indels 4;	Gaps 1

[illegible]

RESULT		8			
BG218214					
LOCUS	BG218214		762 bp	mRNA	linear
DEFINITION	R5737441 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.				
ACCESSION	BG218214				
VERSION	BG218214.1		GI:13744235		
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
1 (bases 1 to 762)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

TITLE	JOURNAL	MEDLINE	COMMENT
Creation of genome-wide protein expression libraries using random activation of gene expression	Nat. Biotechnol.	19 (3), 440-445 (2001)	21227151
Contact: Scott J. Cain			

3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaln@atherys.com
High quality sequence stop: 379.

FEATURES		Location/Qualifiers
Source	1..762	/organism="Homo sapiens"
	/db_xref="taxon:9606"	
	/clone_lib="Athersys RAGE Library"	
	/cell_line="HT1080"	
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."	
BASE COUNT	205 a 165 c 186 g 205 t	1 others
ORIGIN		
Query Match	14.9%: Score 561.2; DB 10; Length 762;	
Best Local Similarity	89.6%: Pred. No. 5.1e-72;	
Matches	682; Conservative 0; Mismatches 69; Indels 10; Gaps 7;	
QY	2635 agtggctcccttgatgagcaaatgctccatcagctgtagatgagatgtaattgtt	2694
DB	2 ACTGATGTTCCCTGGATGGCGAATGCTCATGAGCTGATGATGAGTGTGT	61
QY	2695 accatagacaataatgattatttgggtgtctgaagaatacacacagactgagact	2754
DB	62 ACCCTATGACAAATATGATTTATTTGGTGTCTGAAAGACATACACACAGACT	121
QY	2755 ttttgggagatgagagagctgtagaacaattgctaacaatggtctcttaaa	2814
DB	122 TTTTGGTGAGATCGAGGAGCTGTGATGAACAAATGCTTAACATGAGTCTCTT	181
QY	2815 gaattacccttatgactaccagacatgtgtagagccacaaggaagacagatgagc	2874
DB	182 GATTATACCTTTATGACTATCAAGCCATGTGTAGAGCCACAAGAGAACACGATG	241
QY	2875 ccgatgacctctgtagatccttaaatgctccctctctctgagtaaaatgtagatgacg	2934
DB	242 CCCATGGCTCTCGATCCTTTAATGCTTCTCTCTGACATAAATGATCATGACAG	301
QY	2935 aactgtctgtctctgtagaatttaacctgtagtggtagtgcacatcgatagacg	2994
DB	302 AACTGTCTGTGCTCGGAGGAAATTAACCTTGACGTTGGTGACATCCGATATGAC	361
QY	2995 ctaaaagccagaatgtaaacagaccctgagacctgtagatcctaataccagactcg	3054
DB	362 CTAAAGCCGAGAAATGTAAGAACAGACCTTGAGACCTTGATGATATCCAGCAT	421
QY	3055 tctctgagcgacacatcaagagactacagggatattgtctgtgaagactgtccaa	3114
DB	422 TTTTGAGGCGACCATCAAGGAGACTACAGGATTTTGTGTGTAANACTGTTCA	481
QY	3115 ccttggatccaggaatcccaagcagcaactgttca-tgggtgtgtgtgagcagcag	3173
DB	482 CCTTGTGTGAGAGAAATCCCAACACACACCTGTTCATTTGTTGTTGAGACAG	541
QY	3174 -tgctctgtgtagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3229
DB	542 TTGGCTCTGAGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	601
QY	3230 tgaatcccttaagt-gtgaacgtctaaagccagaagatcagaagagcc-agaac	3286
DB	602 TGGATTCCTTTAATGCGGAACGTCCAAAGGCCAAAGAACAGAGAGGCCGGA	661
QY	3287 ttgtatc-tgcttcaatcctgtagaagaaatgtagaggtgtgtgtgtgtgtgtgt	3345
DB	662 TTGTCTTGGGCTTCACTTCTGAGGAATTTGCAAGAGATGTGTGTGTGTGTGT	721
QY	3346 a-agccacagactcctctctgtcctctgtctgttgaat	3385
DB	722 AAGACCAAAAGGTCTACTTTCTGCTCTCTTGGGTTTGTAT	762

D_b 476 TCGGAAGACTGGTCCAAATCCTTCATTGATCCAGCAAAATCCGAGTAGCAATGTGTTCATG 535
|||||
O_y 3156 qttgttgccttgagacagcagctgcccctctgtgaatctgtggccccaatacattgaccacatc 3215
|||
D_b 536 GTGGTGCTGCACAGTAGCTGTCTCTGTGAAGTCCGGCTCCATAACCATGGCACCCATT 595
|||
O_y 3216 gaatacaaggttaataagaatccctctaagggtgaagtctcaaaagccccbaagatagaag 3275
|||||
D_b 506 GAAATCAGGTATTAATGAATCCCTTAAGTGAACCGTTAAAGGCTCAAGAAGATCCAGACA 655
|||
O_y 3276 cgcaccaaatctctgcatcgcttcacatccatcagaagaaatgacaagggagtgtgtaggttcg 3335
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D_b 656 CGTCCAGAAATCCTGCCACAGG-TTCCATCTCTAAGAGAAATGCAGAAGATGTGGGGTCCA 714
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O_y 3336 ccgaagctctcaaacgccagaacagctccctcctctcgtccctcgtcttlltagtcctcttcca 3395
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D_b 715 TCGAATCTTTACAGGCCCAAGCGGGCTTGCTGCHGCHGCCCTGGTTCCGAGTCTCTTTCAC 774
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O_y 3396 aggtgatcacatgactga 3411
|||||
D_b 775 AGGTGACACTAATACTAA 790
|||

RESULT	10		
BE985092			
LOCUS	BE985092	671 bp	mRNA
DEFINITION	UI-M-CG0p-bdh-c-10-0-0-UI.s1 NIH-BMAP_Ret4-s2 Mus musculus cDNA clone.		linear
	UI-M-CG0p-bdh-c-10-0-0-UI 3', mRNA sequence.		

VERSION	BE9985092.1	GI:10658046
KEYWORDS	EST.	
SOURCE	house mouse,	
ORGANISM	Mus musculus	

REFERENCE AUTHORS TITLE	JOURNAL MEDLINE COMMENT
Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi, Muridae, Mus. 1 (bases 1 to 671)	
Bonaldo,M.F., Lennon,G. and Soares,M.B.	
Normalization and subtraction: two approaches to facilitate gene discovery	
Genome Res. 6 (9), 791-806 (1996)	
9704447	
Contact: Chin, H	

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643 USA
Tel: 301 443 1706
Fax: 301 443 9690
Email: MEStremail.nih.gov
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements.
The following repetitive elements were found in this cDNA sequence:
3-35- >CGGnnSimple_repeat
Seq primer: M13 forward
SOLVA=NO.

FEATURES	Location/Qualifiers
source	1. .671

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UI-M-CGP-bdb-c-10-0-0-UI"
/clone_idb="N1H.BMAP.Ret4.S2"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT7T2-Pic (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
N1H.BMAP.Ret4.S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description

```

BASE COUNT	160 a	164 c	152 t	1 others
ORIGIN				

Query Match	13.7%;	Score 515;	DB 10;	Length 671;
Best Local Similarity	87.8%;	Pred. No. 2.6e-65;		
Matches 599; Conservative	0;	Mismatches 71;	Indels 12;	Gaps 3;

OY	96	cggcgccgtctcgcgcccagcgaggcgctcggaaggaaaccagaatcgcggcgccg	155
Db	1	CGGCGGCTCCATCCCGCGCGCGCGCGCGC-----GCCAGATGGCCGGCGCG	50
OY	156	ggctcgccgcgcgcgcgcgtccccggggggccttcgcgtcttcgcgtcgcgcgtctctctac	215
Db	51	GCGTCGTCTGCTGGCGCGTCCCGGGGGGCCTTGCGGCTCTTAGCCACCGCGCTTCTAC	110
OY	216	ggcgcgccttbggggaagcttgctgcctcgcgaagcaagataccgccttcgcgttgtagaac	275
Db	111	GCGGCTCTGGGGAGACTGTGCGCTTCGAGCACAGCATCCCGCTCTCGTAATGAAGCTG	170
OY	276	tgggcctcgcgcctttggttgggtggaglaaaatccattgcctgcctaagtactccggttccag	335
Db	171	TGGGCTCTCGGCTTTGGTGGGAGATAAATCCATCGCTGCCCAAGTACCGGCGCTCCAG	230
OY	336	ctctgcgcaaaaatatcaaaagafatgaaagaagcgttgtccatagaagaattatagc	395
Db	231	CTTTGTGCAAAACAATACAAAGATGTAGAAGACGTTGCCATTGACAAATTCAGCGT	290
OY	396	ctccacacttggtaaaagaagcttggcaagaacaatgatagaagatgtlctcacagaagctgag	455
Db	291	CTTCCAACGTGGTGAAGAGTTGGCTAAAATCATGGAGGAGATGTTCCACAAAGTCCGAG	350
OY	456	gccgtccaggcgtctcgttggaggctctgcagaagaagcaacacctgaacaatlttatgca	515
Db	351	GGAGTGAGGCGCTTCTGTGAGGCTCAGAGGGGACACCTGAAACATCAATTTATGCT	410
OY	516	gaactacatgaataactccaatgcgtgctgcataaatgaagaagcaaaagcggaaat	575
Db	411	GACTGTGCAGTATGATACTTCAATCTGTCGTGATCAACGANAGGACAAACGCGGAAC	470
OY	576	ttcttggagctvggaaagaaatlcatclctagccccaatlgaccatlttaataattgect	635
Db	471	TTTTTGGAAATTCGGAAGGAA-TCAATCTTAGCCCCCAATTTAATTAATTTGGCT	529
OY	636	gtgaacatcaagctciaagtuaagctccaagtaccaagaagaaatgttacaacaagaacctga	695
Db	530	GTCGAACATCAGTCTGAGTGCATGTGCAAGTGCACAGAACATGTACNACAAAGATCTCGC	589
OY	696	attgtccaatagggttlatatgtgtcgaatctctaaacaagaatttctgtagataacttga-	754
Db	590	AATTGTCAATGGAGTGTANTGTCGTCAATCTCAATCAAAAGTTTGTGGTATCTTGTAT	649
OY	755	ccgtgaccatactctcataatgg 776	
Db	650	CGGGAATTCGTTCTCATATGG 671	

[illegible]

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLNL1932 row: j column: 21
 High quality sequence stop: 709.

FEATURES

Location/Qualifiers

1..711
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 /db_xref="taxon:10090"
 /clone_1ib="MGC_94"
 /clone_1ib="NIH-MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."

BASE COUNT 178 a 185 c 162 g 186 t

ORIGIN

Query Match 13.1%; Score 492.4; DB 10; Length 711;
 Best Local Similarity 89.0%; Pred. No. 4.8e-62;
 Matches 552; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

2736 taacacagacgtgagagacttttgtagatgagagagctgtgatgaacaattgcta 2795
 114 TCCCTACAGACGTGAGATTTTGGAGAGTGAAGAGCTGTCATGAAAGTTGTTA 173
 2796 acaatggtctcttaagaatcacccttaatactgactacaagccatgtgtagaacc 2855
 174 ACATATGGTCTCTTAAATAAATACCTGTAGACATCCAGCCATGTAGAGCCAC 233
 2856 aagaagaagcagagatgagcccatgagccctctgactctataatgactctctgcga 2915
 234 AAGGAGAGCAGTACAGTCCATGACCTCTGAGACCCCTTAAGCTCTTCTCTGCA 293
 2916 gtaaaatgatacagacagactgtctgtcctgtagaatttaacccctcagattg 2975
 294 GCCAAGTGTATGACGAGAACTGTCTTCTCTGCTGAGTTTAACTGTCAGATTGG 353
 2976 tggcactccgatagacagcagtaagaagcagaatgaaacagaccctggagcctgtgat 3035
 354 TGCACTCCACATGACAGCTAAAGCCAGAACTGAACAGACCCGGAACCTTGAT 413
 3036 acggaatcaccagactcgtctgtagcagcacaagaagagactaagggaattgct 3095
 414 ACTGAATACCCAGCTTTGTTCTGAACGACCATCAAGAGACCAAGGAAACATTGCT 473
 3096 tctgaagactgctcaagctctgtcatcacaagaatcccaagcacaacccgttcattg 3155
 474 TGGGAAGACGCTCCCAAGTCTTCGTATCCACAAATCCCGAGTACATCTGTCATG 533
 3156 gtgggtgtgagacagcagctgctctgtgaattgtggcccatcaccatggaaccatt 3215
 534 GTGTGTGTGAGACAGTGTCTCTGTGAGTCCGTGCTCTCTTAACATGAGGACCCAT 593
 3216 gaataagatataatgataatcccttaagtgtgaagcgtctaaagcccggaagatcagaag 3275
 594 GAATACAGGATATGATATCCCTTAAGTGAACGGTTAAAGGCTGCAAGATCAGACGA 653
 3276 cagccagaaatctgtcatggtctcaccagagagagaaatgcaagggtgtgaggtg 3333

Db 654 CGTCAGAAATCCTGCACAGGTTTCACATCTGAGAGATGCAAGAGATGTGGGGTG 711

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

MDLINE

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Query Match 12.7%; Score 479.4; DB 10; Length 589;
 Best Local Similarity 89.4%; Pred. No. 3.8e-60;
 Matches 516; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

2754 ttttggtagatcgaggagcgtgtgatgacaaatgctcaaaatggtgctctttaa 2813
 13 TTTTGGTAGAGGAGGAGAGCTGTCTATGAACAGTTGTTAAACATGCGTTCTTAA 72
 2814 agaattaccctttagctacagccatgctgttagagccaaagaaagcagcatg 2873

[illegible]

source	1..505	/organism="Homo sapiens"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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Oy 3603 gccagtcacgcaaatgaggttggccaca lgataacaccccttcacacagaatgggaccg 3662
|||||
Db 152 gccagtcacgcaaatgaggttggccacatgataatcaccccttcacacagaatgggaccg 93
Oy 3663 caagtggttaggcaagtgccctctgcttgaaacctatgaaaccaaattaaactgtgta 3722
|||||
Db 92 caagtggttaggcaagtgccctctgcttgaaacctatgaaaccaaattaaactgtgta 33
Oy 3723 cttctaaataaagtcataattaaacataaaa 3754
|||||
Db 32 ctttttaataaagtcataattaaacataaaa 1

Search completed: August 16, 2002, 18:17:01
Job time: 8081 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 20:10:25 ; Search time "6.46 Seconds
(without alignments)
1576.185 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667

Sequence: 1 MAGPGSPRRASRGASALAA.....SLQAQTVALLPLLMFSR 1085

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5667	100.0	1085	21	AAV92320
2	5667	100.0	1085	22	AAU01024
3	5667	100.0	1085	22	AAB62248
4	5577	98.4	1065	22	AAU01019
5	5564	98.2	1071	22	AAB62243
6	5459	96.3	1077	22	AAU01026
7	5459	96.3	1077	22	AAB62250
8	5422	95.7	1038	22	AAU01018
9	5422	95.7	1038	22	AAB62242
10	5324	93.9	1019	22	AAU01017
11	5324	93.9	1019	22	AAB62241

12	3515	62.0	1120	21	AAV92321	Human alpha-2-delt
13	3482.5	61.5	1097	22	AAU01038	Human secreted sol
14	3482.5	61.5	1097	22	AAB62262	Human calcium chan
15	3417	60.3	1096	21	AAV92324	Human alpha-2-delt
16	3365	59.4	1069	22	AAU01037	Human secreted sol
17	3365	59.4	1069	22	AAB62261	Human calcium chan
18	3317	58.5	1050	22	AAU01036	Human secreted sol
19	3317	58.5	1050	22	AAB62260	Human calcium chan
20	3123	55.1	1096	21	AAV92323	Human alpha-2-delt
21	2585	45.6	519	21	AAV70460	Human membrane cha
22	1520	26.8	1215	21	AAE02340	D. melanogaster ca
23	1394.5	24.6	2172	22	ABB67958	Drosophila melanog
24	1382.5	24.4	1022	22	AAB62234	Drosophila melanog
25	1376.5	24.3	1191	22	ABB60775	Drosophila melanog
26	1200	21.2	1145	21	AAV92322	Human alpha-2-delt
27	1200	21.2	1145	22	AAU01023	Human secreted sol
28	1200	21.2	1145	22	AAB62247	Human calcium chan
29	1182.5	20.9	1109	22	AAU01016	Human secreted sol
30	1182.5	20.9	1109	22	AAB62240	Human calcium chan
31	1182.5	20.9	1115	22	AAU01025	Human wild type al
32	1182.5	20.9	1115	22	AAB62249	Human calcium chan
33	1154	20.4	1082	22	AAU01015	Human secreted sol
34	1154	20.4	1082	22	AAB62239	Human calcium chan
35	1153.5	20.4	1106	16	AAV73056	Rabbit skeletal ca
36	1151.5	20.3	1091	22	AAU01027	Pig secreted solub
37	1151.5	20.3	1091	22	AAB62251	Porcine calcium ch
38	1148.5	20.3	1106	18	AAW37712	Rabbit skeletal ca
39	1148.5	20.3	1106	18	AAW18389	Rabbit calcium cha
40	1148.5	20.3	1106	21	AAV77545	Rabbit skeletal ca
41	1147.5	20.2	1062	22	AAU01014	Human secreted sol
42	1147.5	20.2	1062	22	AAB62238	Human calcium chan
43	1143.5	20.2	1063	22	AAU01030	Pig secreted solub
44	1143.5	20.2	1063	22	AAB62254	Porcine calcium ch
45	1143.5	20.2	1069	22	AAU01031	Pig secreted solub

ALIGNMENTS

RESULT 1	
AAV92320	
ID AAV92320 standard; Protein; 1085 AA.	
XX	
AC AAV92320;	
XX	
DT 10-AUG-2000 (first entry)	
XX	
DE Human alpha-2-delta-C calcium channel subunit polypeptide.	
XX	
KW alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyrostatic;	
KW anticonvulsant; antimigraine; antiparkinsonian; antidepressant.	
XX	
OS Homo sapiens.	
XX	
PN WO200020450-A2.	
XX	
PD 13-APR-2000.	
XX	
PF 07-OCT-1999; 99WO-US23519.	
XX	
PR 07-OCT-1998; 98US-0103322.	
PR 30-OCT-1998; 98US-0106473.	
PR 29-DEC-1998; 98US-0114088.	
XX	
PA (WARN) WARNER LAMBERT CO.	
XX	
PI Johns MA, Moldover B, Offord JD;	
XX	
DR WPI, 2000-303744/26.	
DR N-PSDB; AAA09253.	
XX	
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D	
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,	

PT anxiety, multiple sclerosis or cancer
 XX
 PS Claim 8; Page 66; 88pp; English.
 XX
 CC The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
 CC The gene has been mapped to chromosome 3p21.1. This gene and the related
 CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells
 CC from abnormal calcium flux by introducing expression vectors containing
 CC the respective gene into mammalian cells. The antisense genes are also
 CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
 CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
 CC Therefore, alpha-delta-2 proteins may also be targeted to treat
 CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
 CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
 CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
 CC addiction syndromes, mood, depression or cancer.
 CC
 XX
 SQ Sequence 1085 AA:
 Query Match 100.0%; Score 5667; DB 21; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGPGSPRRASGASALLAALLVVALGDVVRSEQOIPLSVVKLWASAFGEIKSIAAKY 60
 DB 1 magpgsprrasgsaallaaalllyaalgdvrseqgiplsvklwasafggeklsaaaky 60
 QY 61 SCSQLQKKYEYEDVAIEEDIGLVKKLAKKMEBFHKSEAVRRLVEAEFAHLKH 120
 DB 61 sgsqllqkkyyekdvaleediglvkklakkmeebfhkksaavrirlveaeaaehlkx 120
 QY 121 EEPDADLOYEYNAVILINFRDKGNFLEGEKFEILAPNDHFNNLPVNISLSDVQVPTNNYN 180
 DB 121 efdaddlqeyfnavlinderkdgnflgelkfeilapndhfnlpsnlstdvqvcnmy 180
 QY 181 KDPAIVNGVWSESINKVFNDFRPSLIWQYFGSAGCFRQYPGIKWEPDENGVIAD 240
 DB 181 kdpaivngvwseslnkvfnndfrpsliwqyfgsagcfrrqypgikwepengviad 240
 QY 241 CRNKWYIQATSPKDVYILVDVSGSMKGLRTTKQVSSILDLPGDDDFNNITAYNEE 300
 DB 241 crnkwyigaatspkdvylvdvsgsmkgllrtlkqvtsslldlpgdddfnnilaynee 300
 QY 301 LHVYPCNLGTLYQADRTNKEHFREHLDKLPAKIGMLDIALNEAFNLSDFNHTGOGSI 360
 DB 301 lhvypcngltlyqadrtcnkehrehldklfakgigmldialneafnlstdfnhtggsi 360
 QY 361 CSQAIMLITDGAVDYDTIFAKYMWPRKVRIFTYLLIGREAAFADNLKWMACANKGFTQ 420
 DB 361 csqaimlittdgavdtydtifakymwprkvriftylligreaafadnlkwmacankgftq 420
 QY 421 ISTLADVENMEYLHVLSRKVLDQEHVDVWTEAYIDSTLDDGPRVLMTTVMAPVSK 480
 DB 421 istladvenmeylhvlsrkvldqehvdvwtayidstlddgprvlmttvanpvsfk 480
 QY 481 QNETRSKGIILGVVGTDPVPEKLLKTIKYKLGIVGAFATNNNGYILTHPELRLIYEEG 540
 DB 481 qnetrskgiiilgvvgtdpvpkellktikyklgivgafatnnngyilthpelrliyee 540
 QY 541 KRRKPNYSVDLSEVEDRBDVLRNAVMNRKTKGFSMEYKKTVDKGRVLYMTNDYY 600
 DB 541 krrkpnysvdlsevedrbdvlrnamvnrktkgfsmeykktvdkgrrlyvmtndyyy 600
 QY 601 TDINGTPESLGVALSRRGKATFFRGNTVIEGLHDLHPDVSLADESYCNTDLHPEIRH 660
 DB 601 tdingtpeslglvalsrngkyffrgnvtieeglhdlhpdvsladewyscntdlhpeirh 660
 QY 661 LSOEFAIKLYKGEPLQLQCKELIQEVLFPDVAVSAPTEAWTSALKKSENDSKGVA 720
 DB 661 lsoeafiklykgeplqlqckelilqeavlfpdvavsapieawtsalaksensdkgvea 720
 QY 721 FLGTRTGLSRINLFGAEQLTNDQLAKAGDKENIFNADHFLPMLYRRAAEQIPGSFVSIP 780

DB 721 flgtrtglsrlnlfgaeqltngdflkagdkenifnadhfpmlwyrraaeqipgsfysip 780
 QY 781 ESTGPYNKSNVYTAISTIDLBDRKSPVVAANGIQMKLEFPQRKRTATRQASLDGKS 840
 DB 781 estgpnksnvvtastisidlbdrksppvvaangiomkleafpqrkrtatrqasldgks 840
 QY 841 ISCDDETVCYILIDNNKGFVLESEDYTOTGDPFGEIEGAVMNKLTMGSPKRTTLVDYQAM 900
 DB 841 iscdetvcyilidnnkgfvleseytotgdpfgeiegavmnkltmgsprkrttlvyqam 900
 QY 901 CRANKESDGAHGLDPYNAFLISAVKWIWTELVLVEFNLCSSWMHSDMTJARAQKLQTL 960
 DB 901 crankessdgaahglldpynaflisavkwimtelvlvefnlcsswmhsdmtakagklqtl 960
 QY 961 EPCDREYPAFVSEERITKETTGNIFACEDCSKFVIOQIPSSNLFMVVYSSCCESVAPIT 1020
 DB 961 epcdreypafvseeritketgnifacedcsksfvioqipsnlfmvvdsccicesvapit 1020
 QY 1021 MAPETRYNESLKCERLKAQIRRRPESCHGFPENARECGASPLAQTVLLPLLL 1080
 DB 1021 mapetryneslkerlkagkrrrrpeschgfpenarecgapslqgvtvllllp 1080
 QY 1081 MLFSR 1085
 DB 1081 mlfsr 1085
 RESULT 2
 AAU01024
 ID AAU01024 standard; Protein: 1085 AA.
 XX
 AC AAU01024;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human secreted soluble alpha2delta calcium channel subunit #11 protein.
 XX
 KW Human: secreted calcium channel alpha2delta subunit: alpha2delta-2;
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VCCG;
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
 KW filter binding assay; wheat germ lectin flashplate assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200119870-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WO-EP09137.
 XX
 PR 16-SEP-1999; 99US-0397550.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brown JP, Bertelli F;
 XX
 DR WPI: 2001-235262/24.
 XX
 DR N-PSDB: AAS01414.
 XX
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
 PT Wheat Germ Lectin Flashplate assays -
 XX
 PS Disclosure: Page 94-97; 160pp; English.
 XX
 CC The present sequence represents human secreted calcium channel
 CC alpha2delta subunit #11 which is soluble and retains the functional
 CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labeled gabapentin. The
 CC alpha2delta subunit is 1 of the components of the heteromultimeric

CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel α 1A subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel α 1B subunits (AAU01027-AAU01031) are
CC described. The secreted soluble α 1A subunits may be used in assays
CC (e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-isoleucine,
CC L-Valine, Spermidine and/or L-Phenylalanine) of a calcium channel
CC α 1A subunit.
XX
XX Sequence 1085 AA;

Query Match	100.0%	Score 5667;	DB 22;	Length 1085;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1085; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

Qy	1	MAGGESPRRASRGASALLAAALYALAGDYVRSEOOIPUSVVKIMAEAFGCEITKISAATY	60
Dp	1	magpgsprasrgasalaaallaaalgdvvrseeqipilsuvnlwaseafgceikslaaaky	60
Oy	61	SGSOLLOKKYKEYEKDVAIEEIDGLOLVKTKLAKMMEPMFKSSPAVRLTLEAAEELTKH	120
Dp	61	sgsollqkkyeyekdvaieeidlqlvkvtklakmemeftmkseavrltleeaeaaltkh	120
Oy	121	EPDADLOYEYENALINERKDNFLELCKEEFIAPNDHFNPNLPVNI SLSDVOVPTMYN	180
Dp	121	efeadloyeyenavlinerkdngflelckrefiapndhfnlnpvnislsvdgvptmyn	180
Oy	181	KDPAIUVGVYVSESLNKFVFNDFNRDPSLIMQYTGSAKKFFROYPGI KWEPDENGVIAD	240
Dp	181	kdpaiuvgvyseslnkfvfnfnrdpsliwqygsakgffrqpgikwepdengvialfa	240
Oy	241	CNRNKWTIOATSPKRDVYLVDVSGSKGIRLTAROKTVSSILDTLGDDEDFNITAYNEE	300
Dp	241	cnrnkwtioatspkrdvylvdvsgsmkgirltlaktvssilddtsgdddfnliaynee	300
Oy	301	LHYEPCINGTLVOADRTNKEHFRHLDLKFANGIGMIALDLNEAFNILDFFNHTGOGSI	360
Dp	301	lhyepcingtlvgadrtknehfrhldkifakgigmldialneafnildfndhtggsi	360
Oy	361	CSQAMILITDGAADVTYOTIPAKYVMPWRKRIPIYILIGREAAFRDNI KWMACANKGFFTO	420
Dp	361	csgamiltgdgadvtyotifakymprkripiyiligr eaafrdnikwmacankgfftg	420
Oy	421	ISTLADVOENMYEHLAHSRPRKTVIDOSHVDVMTPEAYIDSTLTLTDGQIVLMTTAPMPFSK	480
Dp	421	istladvoenmyehlhlaspkrvldghdvvmteayidsltlddgqivlmtcvampfsk	480
Oy	481	QNETRSKGILLGVGTDPVPEKELKTLPKYLGIHGAFAITNGVYLTHPELRLLYEEG	540
Dp	481	qnetrskgillgvgtdpvpekelltklpykylghyafaitngvylthpelrlllyeeg	540
Oy	541	KKRRKPWSSVDSLSEVMEBERDVLRLAAMNRRKTKGSKSMVKKTVDIGKAVLYMTNDYY	600
Dp	541	kkrrkpwssvdslevmewdrdvlrlaamnrnkgtksmewkktvdigkavlymntndyy	600
Oy	601	TDIKGTFPFLSCLVALSRHGKFFKFGANTIEGGLHDLHPVSLADKSYCNTDLHPHNRH	660
Dp	601	tdikgtfpflsclvalsrbghyffrgvntlieeglhdlhpvsladensyntdlhpnh	660
Oy	661	LSQLEAIKLYLKGEPILLOCDKEILIOEVLFPDAVVASPIEAYWTSLSAINKSENSDKGEVA	720
Dp	661	lsqleailklylkgepillocckeliegvlfdavvaspieaywtsla:lnksensdkgeva	720
Oy	721	FLGRTGTGRNLNLEVGADQLTNODELAKGKENTFNNDHFRPLWYRRARAEIPSSFYYSIP	780
Dp	721	flgtrgtgrnlnevgaqltnodelfakgkenfnadhrplwyrtraaeipssfyysip	780
Oy	781	FSTSPVKNSSNVVTAJSTIQLDEKKSPPVAAVGIOMLTEFFORFWFVASHQCSASLOKCS	840

[illegible]

RESULT 3

ID AAB62248 standard; Protein; 1085 AA.

AC AAB62248;

DT 11-JUN-2001 (first entry)

Human calcium channel alpha2delta subunit.

KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;

KW nervous system disorder; pain; epilepsy; anxiety; human.

OS Homo sapiens.

PN WO200120336-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09136.

PR 16-SEP-1999; 99US-0397549.

PA (WARN) WARNER LAMBERT CO.

PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

DR WPI; 2001-257902/26.

XX

PT cortical voltage-dependent calcium channel α_2 -delta-1 subunit,

PT nervous system, including pain -

PS Disclosure; Page 93-97; 158pp; English.

CC The invention relates to a new method for screening ligands which bind a

CC preferably alpha2delta-1 subunit. The method comprises contacting a

CC Interest and a labelled compound which binds the subunit, followed by

CC subunit. The method is useful for screening ligands, preferably

CC which bind a cerebral cortical voltage-dependent calcium channel

CC for treating disorders of the nervous system, including pain, epilepsy

CC alpha2delta subunit.
 XX
 SQ Sequence 1085 AA:

Query Match 100.0%; Score 5667; DB 22; Length 1085;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1085; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGPSRRASRGASALLLAALLALGADVRSSEOOPIPLSVKLMSAFGGKIRTAAY 60
 DB 1 magpsrrasrgasalllaallalgaadvrsseqplrsvklmsafggkirsaaay 60
 OY 61 SGGQLQKKYKEYEKDAIEIDGLQVKKLAKNMEEMFKKSEAVRRLVEAAEAAHLKH 120
 DB 61 sggqlqkkkykeyekdaieelidglqvkklaknmeemfkksaavrrlveaaeeahlkh 120
 OY 121 EPFADLQLEYFNAVLINERDKGNFLKKEFLAPNDHFNNL.PVNISLSDVOYPTNNYN 180
 DB 121 efadlqleyfnavlinerdkgnflekfeilapndhfnlnpvnislsvdyvptnnyn 180
 OY 181 KDPATNGVYWSSELNKVFVDFNDPRDPSLIWOYFGSAKGFRRYPGIKWEPDENGVAFD 240
 DB 181 kdpavngvysesslnkvfdndprdrpsliwofgsakgffrpgikwepdengvafid 240
 OY 241 CRNRKMYIOAATSPKDVILLVDYSGSMKGLRLTIKQTVSSIIDTLCDDDFNNIAVNEE 300
 DB 241 cnrkmyioaatspkdvillvdysgsmkgllrtiakqtvsiiidtlcgddffnliaynee 300
 OY 301 LHYVECLNGTLVQADRTNKEHREHLDKLFAKIGMLDIALNEAPNLSDFNNHGGGSI 360
 DB 301 lhyveclngtlvqadrtnekerehldklfakigmlidalneafnlisdfnhtggsi 360
 OY 361 CSQALMLITDGAVDYDTJFAKYNWPDNRKRIPTVYLIGREAFADNLKMAKANKGFQO 420
 DB 361 csqalmlitdgavdydtjfkaynwpdnrkrirptvyligreafaadnlkmaankgffiq 420
 OY 421 ISTLADQENVMEXLHVLNRPKVIDEHDVWMTVETAYIDSTLTDDGSPVLTMTTAMPEFSK 480
 DB 421 istladqenvmexlhvlnrpkvidehdvwmteayidstltddgspvltmttampvfk 480
 OY 481 QNETRKGILLGVNCDVYVKELTKTIPKKGIGRGYAFATNNGYILTHPEIRLLEEG 540
 DB 481 qnetrkgillgvncdvvykelktikpkykighyafatlngyilthpeirlllyeeg 540
 OY 541 KRRRRKPNYSVDLSEVEMEDRDVDLNRNANVRKTKFESMEVKTVDKGKVLWMTNDYY 600
 DB 541 krrrrkpnysvdlsevemedrddvlnrnanvrktkfksmvekvtkvdkgkvlwmtndyy 600
 OY 601 TDIKGTFPSLGVALSNGHKYFFRGNAVTEEGHLDELHPDVSLEDEMSYCNTDLHPEHRH 660
 DB 601 tdikgtfpslgyalsnghkyyffrgnavteeghldelehpdvslademsyscntdlhpehrrh 660
 OY 661 LSOLEAIKILYKGERPLLOCDKLELOEVLFDVAVSAPIEAYWTSIALNSENSENDEKVEVA 720
 DB 661 lsolaeikilykgerpllocdkelleovlfdvavsapieaywtsialnsensendekveva 720
 OY 721 FLGTRTGLSRINLFVGAEOULTNODFLKAGDKENIFNADHPFLYRRAAEQIPISFYYSIP 780
 DB 721 flgtrtglsrlnlfvgaeoultnodflkagdkenifnadhpflyrraaeqipisfysyisip 780
 OY 781 FSTGVPVNSNVVTAISTSIGLDERKSPVVAAGVIOKMLEFFORKEFTWASROCASLDGKCS 840
 DB 781 fstgvpvnsvvtaistsiglderkspvvaagviokmlefforkeftwasrocasldgkcs 840
 OY 841 ISGDETVNCYLIDNNGFLTVSEDTYQTGDFGEIGCAVWNKLLTNGSKRRITLYIQAM 900
 DB 841 isgdetvncylidnngfltvseddyqtgdfgeigevawnmklltngskrritlyiqam 900
 OY 901 CRANKESSGAGGLDPPYNAFLSAVKWIMTELVLFLVEFNLCGSMHSDPTAKOKQKOTL 960
 DB 901 crankeessgaglldppynaflsavkwimtelvflfvefnlcsghsdptakokqkikqtl 960

OY 961 EPCDTEYPAFVSERTIKETTGNIACEDCSKSEFVLIQIPSSNLEPMVVDSSCLCESVAPIT 1020
 DB 961 epcdteypafvserllketignlacedcsksfvlqgipsnllfmvvvdssclcesvapit 1020
 OY 1021 MAPETIRYNESLKCERKAOKIRRRPESCHGFHPEENARECGAPSLQAOVTLLPLLL 1080
 DB 1021 mapetiryneslkerlkaokirrrpeschgfhpeenarecgapslqaovtlllpill 1080
 OY 1081 MLFSR 1085
 DB 1081 mlfsr 1085

RESULT 4
 AAU01019
 ID AAU01019 standard; protein; 1065 AA.
 XX
 AC AAU01019;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human secreted soluble alpha2delta calcium channel subunit #6 protein.
 XX
 KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
 KW filter binding assay; wheat germ lectin flashplate assay.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Msc-difference 1044..1045
 FT /note="Encoded by AGGCCCAAGAATCAGAAGCGC"
 XX
 PN MO200119870-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WC-EP09137.
 XX
 PR 16-SEP-1999; 99US-0397550.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brown JP, Bertelli F;
 XX
 DR MPI: 2001-235262/24.
 DR N-PSDB: AAS01409.
 XX
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT flashplate assays, Nickel flashplate assays, Filter binding assays or
 PT Wheat Germ Lectin flashplate assays -
 XX
 PS Claim 25; Page 79-82; 160pp; English.
 XX
 CC The present sequence represents human secreted calcium channel
 CC alpha2delta subunit #6 which is soluble and retains the functional
 CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labeled gabapentin. The
 CC alpha2delta subunit is 1 of the components of the heteromultimeric
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous
 CC soluble forms of the human calcium channel alpha2delta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
 CC described. The secreted soluble alpha2delta subunit may be used in assays
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
 CC filter binding or wheat germ lectin flashplate assays to detect or
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-Isoleucine, L-mechonine, L-Leucine, L-Isoleucine,
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel

CC alpha2delta subunit.
 XX
 SQ Sequence 1065 AA;

Query Match 98.4%; Score 5577; DB 22; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGPSRRASGASALLAALLYAALGDVVRSEGOIPLSVKLMASAFGEIKSIATKY 60
 DB 1 magpsrrasgasaallaallaalgydvvrseqqiplsvkllwasafgelsiaaky 60
 OY 61 SSSQLQKKYKYEKDVAAIEEIDGOLVKLAKNKEEMHKSEAVRILVEAAEEALKH 120
 DB 61 ssgqlqkkkyekedvaieeidegolvkklaknmeemfhkksavrrilveaaeealkh 120
 OY 121 EFDADLQYEFYNAVLINERDKDNFLGKEPILAPNDHFNNLPVNI:LSDVQVPTNMYN 180
 DB 121 efdaqlqyefynaavlinerdkgdnflgkefilapndhfnlnpvni:lsdvqptnmy 180
 OY 181 KDPALVNGVYWSLUNKYVVDNFDPSLIMQYFGSAKGFQYQYPCIKPEPDENGVIAD 240
 DB 181 kdpalvngvwslnkyvvdnfdpsliwgyfgsakgffqyqyplkwpdengviad 240
 OY 241 CNRRKMYIOAATSPKDVVLIVDVSGSMKGLRLTIKQVTSILDTLGDDEFNIITAYNEE 300
 DB 241 cnrrkmyioaatspkdvvllvdvsgsmkgyrlitlakqvtslldtlgddfnlilaynee 300
 OY 301 LHVYPCNLNGTLVQADRTNKEHFRHLDKLFAGKIGMDIALNEAFNLLSDFNHTGQSI 360
 DB 301 lhyvpcnlngtlvgadrtnkfhrehldklfakgigmldialneafnllsdfnhtgqsi 360
 OY 361 CSQALMLITDGVNRYDITFAKYNNPDRKVRIFTYLIGEAAPADNLKMACANKCFEIQ 420
 DB 361 csqalmlitdgavndydtlfaakynwpdrkvriftyligreaafadnlkmacankcfiq 420
 OY 421 ISTLADVOENVNEYLHVLSRPKVIODEHNVMTYVYIDTFLTDGDPVLMTPYAMPVFEK 480
 DB 421 istladvoenvneylhvlsrpkyidoghovwveayidstltdggpvlmtcvampvfek 480
 OY 481 QNETRSKILLGVGTDPVPEKELKTIPRYKLGINGYAFATNNNGYILTHPELRILEEG 540
 DB 481 qnetrskillgvgtdpvpekeltktpkyklingyafatnngyilthpelrilyeeg 540
 OY 541 KRRKRPNTSSVVLSEVEMEDRDVLRNMAVNNKTGKFSMEVKYTDKGRVLMYNTDYY 600
 DB 541 krrkrpntssvvlsevedrdvlnrnamvnrktgkfsmevktvdkgrvlymntdyy 600
 OY 601 TDIKGTPFSLGVALSRGKGKFFRGKVTVEGLHDLHEDVSLADPKSYCNLDLHPEHH 660
 DB 601 tdikgtpfslgvalsrngkyffrgnvtlleglhdlehpdvsladpksyctndlhpehh 660
 OY 661 LSQLEAIKLYLKGBPLLOCDKELIQEVLEFADVNSAPIEAYMTSLAINSENSDKCEVA 720
 DB 661 lsqleai kylkgbpllqcdkelqevlfeadvnsapieaymtslainnsensdkceva 720
 OY 721 FLGTGTGSLRIULFVGAEDLTQODPLKAGDKENIFNADHFLMYRRAAQIPGSPYISIP 780
 DB 721 flgtgtgslriulfvgadltqodplkagdkenifnadhflmyrraaqipgsfysip 780
 OY 781 FSTGVPVNSNVYTAGSTIOLDERKSPVYAAVGICMKLEFPORKFPTASROCASLDGKS 840
 DB 781 fstgvpvnsnvtagstiolderkspvyaavgicmklefprkfptasrocasldgks 840
 OY 841 ISCDDETVCYLIDNNGFTLVSEEDYTGTGDFEGELEGAVNNKLLTWGSKFRITLYDQAM 900
 DB 841 iscdetvncylidnnngftlvseedytgtgdfegelegavnnklltwgskfritydqm 900
 OY 901 CRANESSDGAAGLLDPYNAFLSAVKWMTLVLVFEFNLCSSWHSMDTAKAKOKTL 960
 DB 901 cranessdgaaglldpynaflsaawkmtlavlfefnlcsswshsmdtakakoktl 960
 OY 901 CRANESSDGAAGLLDPYNAFLSAVKWMTLVLVFEFNLCSSWHSMDTAKAKOKTL 960
 DB 901 cranessdgaaglldpynaflsaawkmtlavlfefnlcsswshsmdtakakoktl 960

OY 961 EPCDTEYPAFVSERTIKETTGNIACEDCSKSFYIQOIPSSNLMFMYVSSCLCEVAPIT 1020
 DB 961 epcdteypafvsertikettgniacedsksfviqoipssnlmfvvssclcevapit 1020
 OY 1021 MADIEIRYNESLKCERLKAKIRRRPESCHGHPDENARECGAP 1065
 DB 1021 madietryneslkcerlkaqkirrpeschgfhpeenarecgap 1065

RESULT 5
 AAB62243
 ID AAB62243 standard; Protein; 1071 AA.
 XX
 AC AAB62243;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Human calcium channel alpha2delta subunit.
 XX
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 XX nervous system disorder; pain; epilepsy; anxiety; human.
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 FT Misc-difference 1041..1046
 FT /note="this region is not indicated in the sequence
 provided in the sequence listing"

WO200120336-A2.
 22-MAR-2001.
 18-SEP-2000; 2000MO-EP09136.
 16-SEP-1999; 99US-0397549.
 (WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chaunan N, Gee NS;
 WPI: 2001-257902/26.
 DR N-PSDB; AAF57546.
 XX
 PT Competitive binding assay for screening ligands which bind a cerebral
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
 PT where the ligands identified are useful for treating disorders of the
 PT nervous system, including pain -

PS Disclosure; Page 79-82; 158pp; English.

XX The invention relates to a new method for screening ligands which bind a
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 CC preferably alpha2delta-1 subunit. The method comprises contacting a
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 CC interest and a labelled compound which binds the subunit, followed by
 CC measuring the level of binding of the labelled compound to alpha2delta-1
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system function,
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are useful
 CC for treating disorders of the nervous system, including pain, epilepsy
 CC and anxiety. The present sequence represents a human calcium channel
 CC alpha2delta subunit.

SQ Sequence 1071 AA;

Query Match 98.2%; Score 5564; DB 22; Length 1071;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

OY 1 MAGPSRRASGASALLAALLYAALGDVVRSEGOIPLSVKLMASAFGEIKSIATKY 60

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Db 1 magpsprsragsaallaaallaaalgydvrsseqjprsvvklwasafgsktsaaky 60
QY 61 SSSQLLQKKYKYEKDVAAIEEIDGLOLVKKLAKNMEEMHKKESEAVRRLVEAEFAHLKH 120
Db 61 ssgqlqkkykkyekdvaaieeIdgIqVkkLaknmeemhkksseavrrlveaeaaahlkh 120
QY 121 EFDADLOEYEFNAVLINERDKGNFLELGKEFTLAPNDHFNNLPVNISLSOVQVFTNMVN 180
Db 121 etfdaIdgyeyfnaVlinerdkgnflelgkeftlApndhfnnlpvnIsldsvqVptmyn 180
QY 181 KDPALVNGVWSESUNKYFVDNFDRDPSLIWQFSGSANGFERQYFGIKWEPDENGIAD 240
Db 181 kdpalvngvwsesInkYfvdnfdrDpsliWqfsgsAngferQyfgIKwepdenGIad 240
QY 241 CRNRKWTQAAATSPKDVTVLVDSGSMKGLRTIAKQVSSLTLDLGDDEFNITAYNEE 300
Db 241 crnrkwtYqaAatSpkdvTVlvdsGsmkglrtIAkqvssLTldlGdddfnItaynee 300
QY 301 LHVPECLNGTLVQADRTNKEHFRHLDKLFAKIGIMLDIALNEAFNILDENHTGQGS 360
Db 301 lhyvpeclngtlvqAdrtNkeHfrhlDKlfAKigIMldIalneaFnildENhtGqgs 360
QY 361 CSQAIMLTTCGAVDTYDTIFAKYNMPDRKVRITFTYLIGREAAFADNLKMACANKGFTQ 420
Db 361 csqaImltTCgavdtYdtIFakYNmpDRkvrITftYLIGreAAfADnlKmacanKgfTq 420
QY 421 ISTLADVOENWEXYHVSRPKVIDEHDVWTFEAYIDSTLTDGDPVLTMTVAMPVSK 480
Db 421 iStladvoenwEXyHvsrPKvIdEhdvWtFeayIdstLTdGdpvLTmtvAmPvSk 480
QY 481 QNETRSKILGLVGTVDPVKELELTKTIPKYLGIHGVAFAITNNGYILTHPELRLLYERG 540
Db 481 qneTrskIlglvgTVdpVkeleLtkTIpKylgiHgvaFAITnngYilThpeLrllYerg 540
QY 541 KRRKRPNSVSDLSVEWEDRDVLRNMAVNRKTGKFSMEVAKTYDKGGRVLYMTNDY 600
Db 541 krrkRpnsvsdlsVEwEDrdVlRnMAvNRktGkfsmEvakTydkGGRvLYmtNdY 600
QY 601 TDIKTPPSLSGVALSRGKGYFERGNVTIEGLHDLHPDVSLADQWSCNTDLPEHH 660
Db 601 tdiKtpPsIsGvalsrGkyfErGnvTleeglhDlhpDvslAdqWscntdlPeHh 660
QY 661 LSQLEAFLYLYKGEBPLQCKELIQEVLFDVAVSAPIEAVYTSALNKSSENSDKGEVA 720
Db 661 lsqleaFlYlykgEBplQckelIqevlfdVvasapiEavYtsalNksensdkgeva 720
QY 721 FLGRTTGSRLNLEFGAEOLTNODFLKAGDKENITNADHFLMYRRAEQIRGSFVYSIP 780
Db 721 flgRtTgsrLnleFGaeOLtnODflKagDKenITnADhflMYrRAeqIRgsfVysIp 780
QY 781 FSTGVNKSNNVYASTSIQLDERKSPVAAAGIOMKLEFPORKMTASROCASIDGKS 840
Db 781 fstgvnksnnvYastSIqlDERkspVaaAGioMklefPorkMTasrocASIdgKs 840
QY 841 ISCDETVNCLIDNNGEFLVSEDTQTGDFEGELEGAVMNKLTMGSFKRTLLDYQAM 900
Db 841 iscdetvnclyIdnNGeFlvseDTqtGdfEGeleGavmnKLtmgsfKrtllDyqAm 900
QY 901 CRANKESSDGAHGLDIPNATLSAVKAMTELVLFLVEFNLCSMHSDMTAAQOLKOTL 960
Db 901 cranKessdGAhGLdIPnaTlsAVkAMteLvlFlvefnlCSmhsdMTAAqOLkOtL 960
QY 961 EPCDEYAFVSEPTIKETTGNIACEDCSKSPVIOQIPSSNLFMVVVOSSCCEVAPT 1020
Db 961 epCdEyaFvsePtIKetTgNiAcEdCSkspVioQIPssnLfMvVVOssCceVapt 1020
QY 1021 MAPLEIRYNESLKCEERLK-----AOKIRRRPESCHGFHPENARECGAP 1065
Db 1021 mapleIryneslKceerLkagkIrrragkIrrpeschgfHpenarecgAp 1071

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AAU01026
ID AAU01026 standard; Protein: 1077 AA.
XX
AC AAU01026;
XX
DT 04-JUL-2001 (first entry)
XX
DE Mouse wild type alpha2delta-3 calcium channel subunit protein.
XX
KW Mouse: secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Mus musculus.
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000MO-EP09137.
XX
PK 16-SEP-1999; 99US-0397550.
XX
PA (WARN ) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI: 2001-235262/24.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays.
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays -
XX
PS Example 12: Page 101-104; 160pp; English.
XX
CC The present sequence represents mouse wild type calcium channel
CC alpha2delta-3 subunit protein which is used to obtain soluble secreted
CC mouse alpha2delta deletion mutant. The sequence is described in an
CC invention relating to truncated alpha2delta-2, alpha2delta-3 or
CC alpha2delta-4 subunit soluble proteins which retain their affinity for
CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the
CC components of the heteromultimeric voltage-dependent calcium channel
CC (VCC) complexes present in neuronal and non-neuronal tissues including
CC heart and skeletal muscle. Numerous soluble forms of the human calcium
CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)
CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits
CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta
CC subunit may be used in assays e.g. scintillation proximity assay (SPA),
CC flashplate, nickel flashplate, filter binding or wheat germ lectin
CC flashplate assays to detect or measure the binding or interaction of a
CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-isoleucine, L-methionine,
CC L-leucine, L-isoleucine, L-valine, Spermine and/or L-phenylalanine) of
CC a calcium channel alpha2delta subunit.
XX
SQ Sequence 1077 AA:

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Query Match 96.3%; Score 5459; DB 22; Length 1077;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1049; Conservative 1; Mismatches 14; Indels 6; Gaps 1;

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QY 1 MAGPSPRRASGASALLAALLAALDGVVSEDOIPLSVYKLTWASAFGCEIKSIKAY 60
Db 1 magpsprsragsaallaaallaaalDgvvrseqjprsvvklwasafgsktsaaky 60
QY 61 SSSQLLQKKYKYEKDVAAIEEIDGLOLVKKLAKNMEEMHKKESEAVRRLVEAEFAHLKH 120
Db 61 ssgqlqkkykkyekdvaaieeIdgIqVkkLaknmeemhkksseavrrlveaeaaahlkh 120
QY 121 EFDADLOEYEFNAVLINERDKGNFLELGKEFTLAPNDHFNNLPVNISLSOVQVFTNMVN 180
Db 121 etfdaIdgyeyfnaVlinerdkgnflelgkeftlApndhfnnlpvnIsldsvqVptmyn 180
QY 181 KDPALVNGVWSESUNKYFVDNFDRDPSLIWQFSGSANGFERQYFGIKWEPDENGIAD 240
Db 181 kdpalvngvwsesInkYfvdnfdrDpsliWqfsgsAngferQyfgIKwepdenGIad 240
QY 241 CRNRKWTQAAATSPKDVTVLVDSGSMKGLRTIAKQVSSLTLDLGDDEFNITAYNEE 300
Db 241 crnrkwtYqaAatSpkdvTVlvdsGsmkglrtIAkqvssLTldlGdddfnItaynee 300
QY 301 LHVPECLNGTLVQADRTNKEHFRHLDKLFAKIGIMLDIALNEAFNILDENHTGQGS 360
Db 301 lhyvpeclngtlvqAdrtNkeHfrhlDKlfAKigIMldIalneaFnildENhtGqgs 360
QY 361 CSQAIMLTTCGAVDTYDTIFAKYNMPDRKVRITFTYLIGREAAFADNLKMACANKGFTQ 420
Db 361 csqaImltTCgavdtYdtIFakYNmpDRkvrITftYLIGreAAfADnlKmacanKgfTq 420
QY 421 ISTLADVOENWEXYHVSRPKVIDEHDVWTFEAYIDSTLTDGDPVLTMTVAMPVSK 480
Db 421 iStladvoenwEXyHvsrPKvIdEhdvWtFeayIdstLTdGdpvLTmtvAmPvSk 480
QY 481 QNETRSKILGLVGTVDPVKELELTKTIPKYLGIHGVAFAITNNGYILTHPELRLLYERG 540
Db 481 qneTrskIlglvgTVdpVkeleLtkTIpKylgiHgvaFAITnngYilThpeLrllYerg 540
QY 541 KRRKRPNSVSDLSVEWEDRDVLRNMAVNRKTGKFSMEVAKTYDKGGRVLYMTNDY 600
Db 541 krrkRpnsvsdlsVEwEDrdVlRnMAvNRktGkfsmEvakTydkGGRvLYmtNdY 600
QY 601 TDIKTPPSLSGVALSRGKGYFERGNVTIEGLHDLHPDVSLADQWSCNTDLPEHH 660
Db 601 tdiKtpPsIsGvalsrGkyfErGnvTleeglhDlhpDvslAdqWscntdlPeHh 660
QY 661 LSQLEAFLYLYKGEBPLQCKELIQEVLFDVAVSAPIEAVYTSALNKSSENSDKGEVA 720
Db 661 lsqleaFlYlykgEBplQckelIqevlfdVvasapiEavYtsalNksensdkgeva 720
QY 721 FLGRTTGSRLNLEFGAEOLTNODFLKAGDKENITNADHFLMYRRAEQIRGSFVYSIP 780
Db 721 flgRtTgsrLnleFGaeOLtnODflKagDKenITnADhflMYrRAeqIRgsfVysIp 780
QY 781 FSTGVNKSNNVYASTSIQLDERKSPVAAAGIOMKLEFPORKMTASROCASIDGKS 840
Db 781 fstgvnksnnvYastSIqlDERkspVaaAGioMklefPorkMTasrocASIdgKs 840
QY 841 ISCDETVNCLIDNNGEFLVSEDTQTGDFEGELEGAVMNKLTMGSFKRTLLDYQAM 900
Db 841 iscdetvnclyIdnNGeFlvseDTqtGdfEGeleGavmnKLtmgsfKrtllDyqAm 900
QY 901 CRANKESSDGAHGLDIPNATLSAVKAMTELVLFLVEFNLCSMHSDMTAAQOLKOTL 960
Db 901 cranKessdGAhGLdIPnaTlsAVkAMteLvlFlvefnlCSmhsdMTAAqOLkOtL 960
QY 961 EPCDEYAFVSEPTIKETTGNIACEDCSKSPVIOQIPSSNLFMVVVOSSCCEVAPT 1020
Db 961 epCdEyaFvsePtIKetTgNiAcEdCSkspVioQIPssnLfMvVVOssCceVapt 1020
QY 1021 MAPLEIRYNESLKCEERLK-----AOKIRRRPESCHGFHPENARECGAP 1065
Db 1021 mapleIryneslKceerLkagkIrrragkIrrpeschgfHpenarecgAp 1071

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QY	181	KDPAIVGVWSSSLKKNVFVNDNDPDSLLIMQYFSGAKKFFRQYRGIMWEPDENVIADF	240
QY	181	KDPAIVGVWSSSLKKNVFVNDNDPDSLLIMQYFSGAKKFFRQYRGIMWEPDENVIADF	240
QY	241	CRNKAKVYIQAAATSPKDVVILIVDSGSMKCLRLTIAKQYSSILIDPLGDDFFNIATVNEE	300
Db	241	CRNKAKVYIQAAATSPKDVVILIVDSGSMKCLRLTIAKQYSSILIDPLGDDFFNIATVNEE	300
Db	241	CRNKAKVYIQAAATSPKDVVILIVDSGSMKCLRLTIAKQYSSILIDPLGDDFFNIATVNEE	300
QY	301	LHVPECLNGTLVQADRTRNKEHREHLDKLFAGIGIMDLIALNEAFNILLSDFNHTGSGSI	360
Db	301	LHVPECLNGTLVQADRTRNKEHREHLDKLFAGIGIMDLIALNEAFNILLSDFNHTGSGSI	360
QY	361	CSQAIMLITPGADVDTDFPAKNWMPDRKVRITFTYLIGREAFADNLMMACANGFTQ	420
Db	361	CSQAIMLITPGADVDTDFPAKNWMPDRKVRITFTYLIGREAFADNLMMACANGFTQ	420
QY	421	ISTLADYQOEVMMEYLHLSRPKVITDDEHVVMTVEAVIDST-----LIDDOGPVLMNTVA	474
Db	421	ISTLADYQOEVMMEYLHLSRPKVITDDEHVVMTVEAVIDST-----LIDDOGPVLMNTVA	474
QY	475	MPVFSKONETRSKGIILGVGTDVPVKELTKTIPKYLIGIHGAPATINNGYILTHPELR	534
Db	475	MPVFSKONETRSKGIILGVGTDVPVKELTKTIPKYLIGIHGAPATINNGYILTHPELR	534
QY	535	LYVEEGKRRKRPVYSSVDLSEVWEEDRDVLRAMVNRKTGKFSMEVYKTYDKRGKRVLM	594
Db	535	LYVEEGKRRKRPVYSSVDLSEVWEEDRDVLRAMVNRKTGKFSMEVYKTYDKRGKRVLM	594
QY	595	TNDYVYNDIKGTFPFLGVALSRHGKGYFFRGVNTIIEGHLDEHDPVCEIADMSKCNIDL	654
Db	595	TNDYVYNDIKGTFPFLGVALSRHGKGYFFRGVNTIIEGHLDEHDPVCEIADMSKCNIDL	654
QY	601	TDNYVDIKGTFPFLGVALSRHGKGYFFRGVNTIIEGHLDEHDPVCEIADMSKCNIDL	660
Db	601	TDNYVDIKGTFPFLGVALSRHGKGYFFRGVNTIIEGHLDEHDPVCEIADMSKCNIDL	660
QY	655	HPEHRHLSQLEAIKLYIKGKEPPLLQCDKELIDQVLFDAVASAPLEAVYTSIALNKSENSD	714
Db	655	HPEHRHLSQLEAIKLYIKGKEPPLLQCDKELIDQVLFDAVASAPLEAVYTSIALNKSENSD	714
QY	715	KGVVATLIGRTGSRNRNLNLPVGEAOLITNDPFLKAGKKNITFNADHPPIWYRRAAOTIGS	774
Db	715	KGVVATLIGRTGSRNRNLNLPVGEAOLITNDPFLKAGKKNITFNADHPPIWYRRAAOTIGS	774
QY	775	FVYSIPSTGPVKNKSNVYVASTSIQDLDERKSPVVAANGIQMKLEFPYRKFTWTASRQAS	834
Db	775	FVYSIPSTGPVKNKSNVYVASTSIQDLDERKSPVVAANGIQMKLEFPYRKFTWTASRQAS	834
QY	835	LJDKGCSISCDDEYVNCYLIDNNGFIIIVSEDDYQTDGFSEIEIGAYVNNKILTMGSKRITL	894
Db	835	LJDKGCSISCDDEYVNCYLIDNNGFIIIVSEDDYQTDGFSEIEIGAYVNNKILTMGSKRITL	894
QY	841	LDGKCSISCDDEYVNCYLIDNNGFIIIVSEDDYQTDGFSEIEIGAYVNNKILTMGSKRITL	900
Db	841	LDGKCSISCDDEYVNCYLIDNNGFIIIVSEDDYQTDGFSEIEIGAYVNNKILTMGSKRITL	900
QY	895	YDYQAMRAKESSDGAGHGLDLPYVNFSLAVKIMELVLFIVERNLSSWMSDMDTAAQ	954
Db	895	YDYQAMRAKESSDGAGHGLDLPYVNFSLAVKIMELVLFIVERNLSSWMSDMDTAAQ	954
QY	901	YDYQAMRAKESSDGAGHGLDLPYVNFSLAVKIMELVLFIVERNLSSWMSDMDTAAQ	960
Db	901	YDYQAMRAKESSDGAGHGLDLPYVNFSLAVKIMELVLFIVERNLSSWMSDMDTAAQ	960
QY	955	KLQKTEPCOTEPAPAFUSERTIKETTGKINACEDCSKSPYIOQIPSSNLPMVVVDSSCCE	1014
Db	955	KLQKTEPCOTEPAPAFUSERTIKETTGKINACEDCSKSPYIOQIPSSNLPMVVVDSSCCE	1014
QY	961	KLQKTEPCOTEPAPAFUSERTIKETTGKINACEDCSKSPYIOQIPSSNLPMVVVDSSCCE	1020
Db	961	KLQKTEPCOTEPAPAFUSERTIKETTGKINACEDCSKSPYIOQIPSSNLPMVVVDSSCCE	1020
QY	1015	SVAPITMAPLEIRYNESLKCEBRLKAOKIRRRPESCHGFPEENARBCGSA	1064
Db	1015	SVAPITMAPLEIRYNESLKCEBRLKAOKIRRRPESCHGFPEENARBCGSA	1064
QY	1021	SVAPITMAPLEIRYNESLKCEBRLKAOKIRRRPESCHGFPEENARBCGSA	1070
Db	1021	SVAPITMAPLEIRYNESLKCEBRLKAOKIRRRPESCHGFPEENARBCGSA	1070
RESULT	7		
AAAB62250			
ID	AAAB62250	standard; Protein; 1077 AA.	
XX	AAAB62250;		
AC			
XX			
DF	11-JUN-2001	(first entry)	
XX			
DE			
XX			
FW			
Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;			

[illegible]

OY	421	ISTLADVENVNEYLHVLSRPVLDQEHDDVWTEAYIDST-----LTDDCGPVLMTTVA	474
Db	421	ISTLADVENVMEYIHLVLSRPVLDQEHDDVWTEAYIDST-----LTDDCGPVLMTTVA	474
OY	475	MPVFSKQNETRSKGLLVGVGTDPVPEKLLKTIPEKKYLGINGVAFATINNGYILTHBELR	534
Db	481	mpvfakqnetrskglllgvgvgtdivpvekllktlpekykligingvafatlnngyilthpeldr	540
OY	535	LLIEEGKKRRKRNYSVVLSEYEWEDRDVLRNMAVNNKTKRFSMEYKKYTDGGRVLVM	594
Db	541	plyeegkkrrkrpnyssvvlsevewedrdvlnnamvnrkcgkfsmeykkltydkgkrylvn	600
OY	595	TNDYVYTDIKGPFSLGVALSGHKCYFFRCGNVTIEEGELHOLEHPDVSILAEMWGYCNTD	654
Db	601	tnndyvttdikgpfslgvalsrghnkyffrgnvtleeglhnlhepdsiladewycntdl	660
OY	655	HEPHRLSQLEAIKLYLKGEKPELDQCEKELIQEVLFDVAVSAPIEAVYTSIALNKSENSD	714
Db	661	hpehrlsqleaiiklylkgepeldqckelldqevlfddavsaapieaytsialnksensd	720
OY	715	KGVFAFLGTRGSLRNLPFGAEGLTQDPLKAGDKENITNADHFLMYRRAAEQIPGS	774
Db	721	kgvfaflgtrtgsrlnlpfgaegltnqdpflkagdkenitnadhfplmyrraaeqiags	780
OY	775	FVYSIPEFTGPVRNKSNNVTASTSIDLDERKSPVYAAVGIDMKLEFQORRPMTASRCCAS	834
Db	781	fvyssipectgvrnknnvvtastsidlderspyvaavgidmkleffqkrfwtsrqcas	840
OY	835	LDGKCSICDDETVNYCYLIDNNGFLLVSEDDYTQTGDFEGELIGAVMKNKLMTGSEFKRITL	894
Db	841	ldgkcsicddetvncyilidnngfllvseddytlqctgdfegevagvmklltmgsfkritll	900
OY	895	VDYQAMCANKNESSGAGGLLDPRVAFSLAAYKMTETLYELFVFNLCSMWHSMTAKAQ	954
Db	901	vydqamcanknessagsanglldprvafslsaakwlmtevltyelfvfnlcswwhsmdtaq	960
OY	955	KLKQGLPECDTEYPAFVSEERTIKETTCGNIACEDCSKFVIOQIPSSNLFMVVDSQCICE	1014
Db	961	kklqglpecdteypafvseertiketnctgniacedcsksfviqipssnlfmvvdsqcice	1020
OY	1015	SVAPITMAPIEIRVNESLKCERLKAQKTRRRPESCHGFHPENARECGGA	1064
Db	1021	svapitmapieirvneslkcerlkqaktrrrpeschgfhpenaarccga	1070
RESULT 8			
AAU01018			
XX	ID	AAU01018 standard; Protein; 1038 AA.	
XX	AC	AAU01018;	
XX	XX		
XX	DT	04-JUL-2001 (first entry)	
DE	XX	Human secreted soluble alpha2delta calcium channel subunit #5 protein.	
XX	XX		
KW	XX	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;	
KW	XX	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;	
KW	XX	gabapentin; schinlilation proximity assay; SPA; nickel flashplate assay;	
XX	XX	filter binding assay; wheat germ lectin flashplate assay.	
XX	OS	Homo sapiens.	
XX	PN	W0200119870-A2.	
XX	PD	22-MAR-2001.	
XX	PF	18-SEP-2000; 2000WO-EP09137.	
XX	PR	16-SEP-1999; 99US-0397550.	
XX	XX		
XX	XX	(WARN) WARNER LAMBERT CO.	

PI Brown JP, Bertelli F;
XX
DR MPI: 2001-235262/24.
N-PSDB: AAS01408.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel flashplate assays, Filter binding assays or
XX Wheat germ lectin flashplate assays -
PS
XX
Claim 25: Page 75-79; 160pp: English.
CC
CC The present sequence represents human secreted calcium channel
CC alpha2delta subunit #5 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labeled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-isoleucine,
CC L-valine, Spermine and/or L-phenylalanine) of a calcium channel
CC alpha2delta subunit.
XX
Sequence 1038 AA;
SQ

Query Match	Similarity	95.7%	Score	54.22	DB	22	Length	1038
Best Local	Similarity	100.0%	Pred. NO.	0				
Matches	1038	Conservative	0	Mismatches	0	Indels	0	Gaps
OY	1	MAGPSPRRASGAGALLAALALYALGADVNSEDOIPLSVYKILWASAFGEIKSIATAKY	60					
Db	1	magpsprrasgaaallaaelllyaalgdvvrseqgiprsvklwasatgsktslaey	60					
OY	61	SGSQLQKKYKEYEKDVAIEEIDGQLYKKLKKNMEFHKKSEAVRRLVEAEAHLLKH	120					
Db	61	sgsqllqkkkykeyekdvaieeIdgIqlvklaknmeemfhkksseavrrlveaeaaahllkh	120					
OY	121	EPDADLOVEYFAAVILINERDKDNFLEIGKEPILANPHFNFLPVNISIDVQVPTNMN	180					
Db	121	eIdaadIqYeyIaavIlIneDkDgnIlElgkElIapndIInlPvnlSIdqvPnmn	180					
OY	181	KDPAIVNGVYWSSEINKYFVDNFRDPSLIIMQYFESAGGFRRQYGIKWEPDENCVAFD	240					
Db	181	kDpaIvngYwSseInkYfVdnFRdpsLIImQYfEsagGfRRqYgIKwepDengvIafD	240					
OY	241	CNRKRWYIOAATSPKDVVILNDVSGSMKGLRLTIKQTVSSILDLRGDDDFNITAYNEE	300					
Db	241	cnrkYwYIqaatSpkdvVIlNdVsgSmkGlrLTIakQTVssIlDlrgDddfnIaYnee	300					
OY	301	LHYEPCINGTLVQADRNKKEHREHLQKLFKKGIMDIALNEAFNITSDENHNGGCSI	360					
Db	301	lHyepCIngtlVqadRnKkEHrEhLQkLfKkGImDIAlNEaFNITsdEnhNgGcsI	360					
OY	361	CSOAIMLITDGAVDVDTITFAKYNMPPDRKVRITFTYLIGREAAFAONLMMACANKGFTQ	420					
Db	361	csqaImIlItDgaVdVdItfakYnmPdrKvrItfTylIgreaaFadnLkMcaanGfTq	420					
OY	421	ISTLADVOENWEYIHLVLRPKVIODEHDVWTEAY IDSTLTDDGQPVLMTTVAMPFSK	480					
Db	421	IstlAdvOenWeyIhLvLsrPkVIOdeHdVwTeayIdStlTddGpVlmttVampfSk	480					
OY	481	QNEPFSKGIILGVGTVDPVKELLTIIRKYLGIHGVAFAFATNNQYILTHRELRILYEEG	540					
Db	481	qneIpskGIILgvGtVdpVkeLlTIrKylGIhGvAFaFATnNQyIlThreLrIlYeeG	540					

Oy	541	KKRRKPNVSSDLSSEVMEERDROVLNANMVRKKTGFSMEYKKTIDKCKRVLVMTNDYY	600
Oy	541	KKRRKPNVSSDLSSEVMEERDROVLNANMVRKKTGFSMEYKKTIDKCKRVLVMTNDYY	600
Db	541	KKRRKPNVSSDLSSEVMEERDROVLNANMVRKKTGFSMEYKKTIDKCKRVLVMTNDYY	600
Oy	601	TDIKGFPEFSLGVALSRHGKVFPRFGNVTIIEEGJLHDEJHDPVSLADPKVSCNTDLPERRH	660
Db	601	TDIKGFPEFSLGVALSRHGKVFPRFGNVTIIEEGJLHDEJHDPVSLADPKVSCNTDLPERRH	660
Oy	661	LSQLEAIKLYLKGEKPELLQCDKELIQEVLFDVAVSAPIEAYWTSIALKSENSDKGEVA	720
Db	661	LSQLEAIKLYLKGEKPELLQCDKELIQEVLFDVAVSAPIEAYWTSIALKSENSDKGEVA	720
Oy	721	FLGRRTGSLRNLFVGAEOJLTNDQFLKAGDKKEIFNADFPPLMYRRRAEQIPGSFVYSIP	780
Db	721	FLGRRTGSLRNLFVGAEOJLTNDQFLKAGDKKEIFNADFPPLMYRRRAEQIPGSFVYSIP	780
Oy	781	FSTGPVKSNVWVASTSTIOLDBERKSPVVAAGVIOKLEFFPORKFWTYSROCASLDGKS	840
Db	781	FSTGPVKSNVWVASTSTIOLDBERKSPVVAAGVIOKLEFFPORKFWTYSROCASLDGKS	840
Oy	841	ISCDDETVCNLYLDNNGFIIIVSEDYQTQDGFEGEIGCAVMNKLITMGSEFKRTLLDYDAM	900
Db	841	ISCDDETVCNLYLDNNGFIIIVSEDYQTQDGFEGEIGCAVMNKLITMGSEFKRTLLDYDAM	900
Oy	901	CRANKESDDAGHGLDPRYNAFLSNVKNIMELVLFVERNLCSSWHSDMTAKAOKLKOTL	960
Db	901	CRANKESDDAGHGLDPRYNAFLSNVKNIMELVLFVERNLCSSWHSDMTAKAOKLKOTL	960
Oy	961	EPCTEPAFAFSERTIKETTGNIACEPCKSPFVIOQIPSSNLFMYVVDSSCCESVAPTT	1020
Db	961	EPCTEPAFAFSERTIKETTGNIACEPCKSPFVIOQIPSSNLFMYVVDSSCCESVAPTT	1020
Oy	1021	MAPIEIRYNESLKGERLK 1038	
Db	1021	MAPIEIRYNESLKGERLK 1038	
RESULT	9		
AAB62242	ID	AAB62242 standard; Protein; 1038 AA.	
AC	AAB62242:		
XX	11-JUN-2001	(first entry)	
DE	Human calcium channel alpha2delta subunit.		
KW	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;		
KW	nervous system disorder; pain; epilepsy; anxiety; human.		
OS	Homo sapiens.		
XX	MO200120336-A2.		
PN	22-MAR-2001.		
PD	18-SEP-2000; 2000MO-EP09136.		
PF	16-SEP-1999; 99US-0397549.		
PR	(WARN) WARNER LAMBERT CO.		
PI	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;		
XX	WPI; 2001-257902/26.		
DR	N-PSDB; AAF57545.		
XX	Competitive binding assay for screening ligands which bind a cerebral		
PT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit,		
PT	where the ligands identified are useful for treating disorders of the		
XX	nervous system, including pain -		

PS	Disclosure:	Page 76-79; 158pp;	English.
XX	CC	The invention relates to a new method for screening ligands which bind a	
XX	CC	cerebral cortical voltage-dependent calcium channel alpha2delta subunit,	
CC	CC	preferably alphasdelta-1 subunit. The method comprises contacting a	
CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand of		
CC	interest and a labelled compound which binds the subunit, followed by		
CC	measuring the level of binding of the labelled compound to alphadelta-1		
CC	subunit. The method is useful for screening ligands, preferably		
CC	biologically active products that modulate a nervous system function,		
CC	which bind a cerebral cortical voltage-dependent calcium channel		
CC	alphadelta-1 subunit. The ligands identified by the method are useful		
CC	for treating disorders of the nervous system, including pain, epilepsy		
CC	and anxiety. The present sequence represents a human calcium channel		
CC	alpha2delta subunit.		
xx	Sequence	1038 AA;	
SQ			
	Query Match	95.7%; Score 5422; DB 22; Length 1038;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1038; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MAGPSPRRASGASALLAALVLAALGVNVEEQIPLSVYKLMASAGEIKSIAYKY	60
Dd	1	magspsrrasrgasaallaalvyaalgvnvseqqiplsvyklwasatfgelgsiaaky	60
QY	61	SSQLLÖKKYKEYEKDVAIEETIDGLQLVKKLAKNMENMHKSSEAVRLYEAEHNLK	120
Dd	61	sqsqllökkkykeyekdvaaieetidqlvkkalaknemeahkksseavrrlyeaeeahlkh	120
QY	121	EEDPADLOYYEFAVALINEEDKGNFELCEKEFLAPNDHFNNILPVVISLSDOVPNNMYN	180
Dd	121	eidedadlgyeyfnavilinedkgnfelgkeflapndhfnnlpnisistdqvpncmyn	180
QY	181	KDPALVNGVWSESLEKNFVDNFDSDSLIMOWFGSAGCFPROGCIKWEPDNQVIADP	240
Dd	181	kdpalvngvweseslnkfvdnfdsdslimwfygsagcfrpogciakwepdnqvaiadp	240
QY	241	CNRNKRYIOAAISPKDVYLIVDSGSMKLRTIAQOTYSITLDPTGGDDPFNIATVNEE	300
Dd	241	cnrnryiqaaaispkdvylivdsgsmklrtliaqotysitldtggddfnillaynee	300
QY	301	LHYVEPCNLGTVOADRTNKEHFRHLDLKLFAGIGMDIALNEAFNISDENHTGOGSI	360
Dd	301	lhvepcnlgtlvoadrtnkehfrhlclklfagjgmldialneafnilsdfnhtggsi	360
QY	361	GSOAIMLTIDGADVDTITFAKYINMPDRKVRIFTYLIGEBAFPADNLKMAACANKGFPO	420
Dd	361	cgsoaimltidgadvdtitfakynmpdrkvritftylligreeafadnlkmaacankgyffq	420
QY	421	IETLADVOENWMEYLHVLSRPVYIDDEHPVWT EAYIDSTLTPDDGCPVLMTYVAMPVSF	480
Dd	421	ietladvgenwmeylhvlsrpkyidghhpvtteayidsltiddgcpvlmtcvampvfefk	480
QY	481	QNETSRSKILLVGVTGPVKELKTIPYKLGIGHYAFATNNNGYILTNPBLRLLYEEG	540
Dd	481	qnetsrskgillvgvtdgpvkelltkipryklighyafatinnnyiltphelrllyeeeg	540
QY	541	KRRRPNVSSVDSLSEWEMDRDDVLRBNANVNKRCTGESEMKVTKYDGKGRVYVMNTDYX	600
Dd	541	krirpnvssvdlsewedrdovlrbnanvnkrctgfisemvktvydgkgrvlyvmntdyxy	600
QY	601	TDIKGTPEFLGALSNGHKYFFRGNVTLTEEGJLHLEHEDVSLADEWSYCNTDLPHBRH	660
Dd	601	t dikgtpeflgalsnghkyyfrcgnvltteegjlhlehdvsladeswycndlphbrh	660
QY	661	ISQLAIRKIYLLGKEPRLCDDKEELLDEVLPDAVNASPIATYNTSLANKSENSDSGVEYA	720
Dd	661	isqlaairkiylkgkepirlcdckelldevlpdavnaspiatayntslnksenstdsgyveva	720
QY	721	PFGTGTGSRIMLFWGAEOULTMODFLKADCKNIFENADIFFPLMYRAAQOIGSEFYVSTP	780

Db	841	iscdelvncylidnngfilvseydtyctgtdffgeiegavmknllimg;fkrtllydyqam	900
Qy	901	CRANNESSDGAHGLDDPNAFLSAVKWIMTELVLFVEFNLCSMWHSIMTAKAQIKOTL	960
Db	901	crankeessdgbnllldpynafisavkwimtelvlfvefnlcswhshmtakagllkqll	960
Qy	961	EPCDIEFAFVSERIKETGTGNINACEDCSKSFVIOQIFSSNLFMYVYVSSCLCESVAP	1019
Db	961	epcdiefaivseriketgtgnlacedcsksfviqilpsnlfmvyvssclcesvapl	1019
RESULT 11			
ID	AAB62241	standard; Protein; 1019 AA.	
XX	AC	AAB62241;	
XX	DT	11-JUN-2001 (first entry)	
DE	XX	Human calcium channel alpha2delta subunit.	
KW	XX	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;	
KW	XX	nervous system disorder; pain; epilepsy; anxiety; human.	
OS	XX	Homo sapiens.	
PN	XX	WO200120336-A2.	
PD	XX	22-MAR-2001.	
PE	XX	18-SEP-2000; 2000WO-EP09136.	
PR	XX	16-SEP-1999; 99US-0397549.	
PA	XX	(WARN) WARNER LAMBERT CO.	
PI	XX	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;	
DR	XX	WPI: 2001-257902/26.	
XX	XX	N-PSDB; AAF57544.	
PT	XX	Competitive binding assay for screening ligands which bind a cerebral	
PT	XX	cortical voltage-dependent calcium channel alpha2-delta-1 subunit,	
PT	XX	where the ligands identified are useful for treating disorders of the	
PT	XX	nervous system, including pain -	
PS	XX	Disclosure: Page 72-75; 158pp; English.	
CC	XX	The invention relates to a new method for screening ligands which bind a	
CC	XX	cerebral cortical voltage-dependent calcium channel alpha2delta subunit,	
CC	XX	preferably alpha2delta-1 subunit. The method comprises contacting a	
CC	XX	secreted soluble recombinant alpha2delta-1 subunit with a ligand of	
CC	XX	interest and a labelled compound which binds the subunit, followed by	
CC	XX	measuring the level of binding of the labelled compound to alpha2delta-1	
CC	XX	subunit. The method is useful for screening ligands, preferably	
CC	XX	biologically active products that modulate a nervous system function,	
CC	XX	which bind a cerebral cortical voltage-dependent calcium channel	
CC	XX	alpha2delta-1 subunit. The ligands identified by the method are useful	
CC	XX	for treating disorders of the nervous system, including pain, epilepsy	
CC	XX	and anxiety. The present sequence represents a human calcium channel	
CC	XX	alpha2delta subunit.	
SO	Sequence	1019 AA;	
Query Match 93.9%; Score 5324; DB 22; Length 1019;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MAGPSSPRRASGASALLAALLYALADGVNASEOQIPLSYVKWASAGGEGIKSIAMRY	60
Db	1	magpssprrasgasaalllaalllyaalgdvvrseqdiplsyvkwasatggselksiaaky	60

QY	61	SGSOLLQKKYKEYEKDAVIAEEDGLQVKKLAKMMEKPHKSPAVRRLYEAABEALKH	120
Db	61	sgsqllqkkkykeyekdvaieedglqvkkklakmmeemfhkksaavrrilveaaeeahlk	120
QY	121	EEPDADLOEYENAVLIINERDQKGFLELGEKFLIAPDHFNPNLIPVNIISLDVQYPTMYN	180
Db	121	etdaadlqyeyfnaavliinerdkdgnflteqkerflapdhfnlnpvnislsvqyprctmyn	180
QY	181	KDPAIVNQVWVWSESINLKVFVNPNFRDPSLIHQVFGSAKGFEROYPGIWKPEDENGVIAFD	240
Db	181	kdpaiavgvwvwseslnkvfnvnpfrdpslihqvfgsakgfferoypgiwpkpepdeavgiafd	240
QY	241	CRNRKRWIOAATSPKDVVILVDVSGSMKGLRLTIAKOTVSSILDTLCDDDFPNIIAYNEE	300
Db	241	crnrkwyigaatspkdvvvlvdvsgsmkgjrltliakqtvsilddtlcgdddfnnliaynee	300
QY	301	LHYEPCINGFLVQADRNRKHEFHEDDKLFAKQITGMILDALNRAFNILSDFNHTGGSI	360
Db	301	lhypcpcingltvqadrtnrkhefheddklfakqitgmildalnrafnilsdfnhtggsi	360
QY	361	CSOAFMLITDCAVDPDYDIFPKYMWMPDRKVRIFPYLLGREGAFAFADNLKMMACANKGFQTQ	420
Db	361	csgaamlitdgavdtydifikymwmpdkvrifpyllgreaafadnlkmmacankgffqtq	420
QY	421	ISTLADVOENMEYLHLVSRPKVIDQEHDDVWTEAYIDSTLTDDQGFVLTMTVAMPYFSK	480
Db	421	istladvgenmeylhlvlsrpkvidqehdvwteayidsltddqgfvltmtvampfsk	480
QY	481	QNETSKSILLGVGTVDPVKEELKTRPKYKLGSHGAFAATTNNGYILTRPELRILYEEG	540
Db	481	qnetksklllgvgtdvpvkeellktrpkylgshgafaattnngyiltrpelrillyeeg	540
QY	541	KRRKPNVSVYDLSEVEEDEDVDVLRNANVNRKSGKSMEMKRVYDGGKRVLVMTNDYU	600
Db	541	krkpnvsvydlseveeeddvdlrnanvnrksgksmekrvydgdkrvlvmtndyuy	600
QY	601	TDIKTPTSLGVALSRGHGKFFRGKNVITIEGLHDLDEHPDVSIADEMSYCNTDLNPRENRH	660
Db	601	tdiktptslgvalsrghgkffrgknvitiieglhdldehpdvsiademsyscntdlnprenrh	660
QY	661	LSQLEAIRLYLKGEPELLQCKRELIOEVLFPYAVVSAPLEATWTSIALNKSENSDKGEVA	720
Db	661	lsqleairlylkgepellqckrelioevlfpavvsapleatwtsialnksensdkgeva	720
QY	721	FLGTPTGSLRNLNLPGAROLNODPELKAQKDENFENDHPLEWRRABEOIPGSEFYVSI	780
Db	721	flgtptgslrnlnlpgarolnopedelkaqkdenfendhplewrraboiipgsefyvsi	780
QY	781	FSTGVPNKSNNVTASTSTQLLDERKSPYAAVAGIOMKLEFFORFXTWASROCASLSDKCS	840
Db	781	fstgvpnksnnvtaststqllderkspyaavagiomklefforfxtwasrocaslsdkcs	840
QY	841	ISCDDEFVNCYLIDNNGFVLVSEDTYOTGDFFGEIEGAVNMKLLTWGSEFKRILLYQAM	900
Db	841	iscddefvncylidnngfvlvseddyotgdffgeiegvnmklltwgsefkrillyqam	900
QY	901	CRANKESDGAHGLIDPVNATLSAVKMTMTLVLFIIVEFNLCSMWHSDMKAAQKLOTL	960
Db	901	crankestdgainglidpvnatlsavkmtlvtlfiivefnlcswhsdmkaaklqcl	960
QY	961	EPCDTEYFAFVSEPTIKETTNICAECDSSKFVVIQOIPSSNLFVWVDSGCLCEBVA	1019
Db	961	epcdteyefavseptikettnicaecdsskfvviiqoiipssnlfvwvdsclcebv	1019
RESULT 12			
AA92321			
XX	AA92321	standard; Protein: 1120 AA.	
XX	AA92321:		
XX	10-AUG-2000 (first entry)		
XX			

xx Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
xx
xx WPI; 2001-257902/26.
DR
xx
xx Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
xx
xx
PS Disclosure: Page 154-157; 158pp; English.

xx The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit.
xx
xx

SQ Sequence 1097 AA;

Query Match 61.5%; Score 3482.5; DB 22; Length 1097;

Best Local Similarity 60.0%; Fred. No. 1e-286; Mismatches 217; Indels 15; Gaps 7;

Matches 638; Conservative 194; Mismatches 217; Indels 15; Gaps 7;

QY 15 SALLAALLLYALGDVNSEQIPLSVVYKLMASAFGEIKSIKAKYSGSOLQKKKEYE 74
DB 34 sallllllllygclslp-awgqekipletvklwadtfggdlyncvtvysglllqkkykdv 92
QY 75 KDVAIEETIDGLOLVKLLAKMEEMFHKSSEAVRLVEAAEAAHLNEFDADLOEYFNAY 134
DB 93 salkleevdgletlvrkfseadmenlrkveaqvnlveaaeaaadlnhefneslvfdynav 152
QY 135 LINEBDKGNFLELGKEFLIAPNDHNNLPVNISLSDQVPPNNMKDQATYNGYVMS 194
DB 153 llnedkgnflevlgaelilnesanhtsnprvtslssvqrlpnyvkkpdlngyvmsea 212
QY 195 LNKVFNDFNDRDPSLIWQYFGSAGFFROYPGIKWEPDENGVIAIDCRKRYIAATSP 254
DB 213 lnavfvenfgdprlrltwqyfgsagtflllypgikwtrpdenqvtltdcnnrgyigaet 272
QY 255 KDVVLVNVSGSMKGLRLTIKQVSSILDTLGGDDFFNIAYNEELHAYVEPCLNGTLVQ 314
DB 273 kdlvllvngvsgmkglrltiakqvtssiltdltdlgenfynllyayndvhylerpcfkgllvq 332
QY 315 ADRTKKEHREHLDFKKGIGMLDIALNEAFNLSDFNHTGSGISGATMLITDGAAND 374
DB 333 adrtkrehfkllveelmkvgvavdgatreaqlkqfgeakgslcmgahtlisdgave 392
QY 375 TYDTIFAKYNNPDRKVRITFTYLGREAFAADNLKMACANKGFFQISTLADVOENVEY 434
DB 393 dyepfeykynpdcvkvrftyligrevfadtcmkacnkytqdistledtgenmey 452
QY 435 LHVLSRPKVIOQEHVDVTEAVYIDSTLTDDGP--VLTMTVAMPVFSKONETRSKGIILG 492
DB 453 lhvlsrpnvlhndhllvceaymdeklissqgsaltiltvtampvfksknetrshglllg 512
QY 493 VVGTDVPVKELTKTKPKKGLHGCAFAITNNGYILTHRELRLLYEEGKK--RRKNYSYV 551
DB 513 vvgtdvavtrelmkklaprklyghyaflnctngyllshpdlrplyregkklpkpnyhsv 572
QY 552 DLSEVEMEDRDVLRNNAVNRKTKFSMEVKTKVDKGRVLVMTDYTYTDTKGPFSIG 611
DB 573 dlsevewedqeslrtnmtntetgltlmdvkvymdkgrvflftndyftldstclpfslg 632

QY 612 VALSRGCHGYFRFGVNTVIEGLDHLDEHPDVSLADEMSYCNTRLHPERHLSOLEATKLYL 671
DB 633 vlvsrghgylllgnstsvveghldhllpdlatalagdwlycltdldpdkrlslsqeamltrfl 692
QY 672 KGKEPLOCDDKELIOEVLEDAVVSAPIEAVYWSLANKSENSDKGVAFGLGR--TGLSR 730
DB 693 tkdkploedeevltrevlildavvtapmeayvtalalmseeeshvvdmaflgltasglllr 752
QY 731 INLFVGAEOFLTQMODFLKAGDKENIFNADHFPILYRRAAOIRGSEFYYSIPFSTGP--VNR 788
DB 753 sslfygsekvstklftpedeasvfltdrlfplyrqdashpagsvfnrlrweegpesage 812
QY 789 SNVYVASTSIQLDERKSPVVAAGIOMKLEFFQRRKWTASQACSLDKCSISCODETV 848
DB 813 pmvltastavavtdvkrtaalaaaygmkllefqrkfwatrtqstevdpcqcsedsl 872
QY 849 NCYLDINNGFIIIVSEDTOTGDFEGEIEAAYNNKILLTMSFRRITLYDQACRANKES 908
DB 873 dclvldnngflllskstrctgrflgevdgavltqlismvgfsqvtmlydymckpshhh 932
QY 909 DGAHGLDPYNAFLSAVKWIMTELVLVEFNLCS--SMHSDMTAKA-----QKLKQYL 960
DB 933 saagrlvpslaltcatrlllgelvfllewsvgsvydrgaeksvfnshkhkqdp 992
QY 961 EPCDTEYPAFVSERTIKETTGNIACEDCSKSFVIOIPSSNLFMVYVSDSCLESAVPI 1020
DB 993 gpcdteyprfyvypalrtreanglvecgpcqkvfvgqqlpnslllvtldptcdslfprvl 1052
QY 1021 MAPIEIRYNESLKERLAKQKTRRRPESCHGFHPRENAECGGA 1064
DB 1053 gateevkkyasvkcdrmsqklrrtpdschafpneaqdcgga 1096

RESULT 15

ID AAY92324 standard; Protein; 1096 AA.

AC AAY92324;

DT 10-AUG-2000 (first entry)

DE Human alpha-2-delta-D polypeptide from splice variant 1.

KW alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytosolic;

KM anticouversant; antimigraine; antiparkinsonian; antidepressant;

OS splice variant.

OS Homo sapiens.

PN WO200020450-A2.

PD 13-APR-2000.

PE 07-OCT-1999; 99WO-US23519.

PR 07-OCT-1998; 98US-0103322.

PR 30-OCT-1998; 98US-0106473.

PR 29-DEC-1998; 98US-0114088.

PA (WARN) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Offord JD;

DR WPI; 2000-303744/26.

DR N-PSDB: AAA09729.

XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D

XX proteins, useful in the treatment of epilepsy, migraine, chronic pain,

XX anxiety, multiple sclerosis or cancer

PS Example 3; Page 73; 88pp; English.

CC This alpha-2-delta-D polypeptide is encoded by a splice variant that

.....

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 20:11:25 ; Search time 73 Seconds
(without alignments)
363.038 Million cell updates/sec

Title: US-09-787-657-5
Perfect score: 5667
Sequence: 1 MAGPGSPRRASRGASALLAA.....SLAQGVLLPLLMFSR 1085

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/CTOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1148.5	20.3	1106	US-08-435-675B-5	Sequence 5, Appl1
2	1148.5	20.3	1106	US-08-336-257A-8	Sequence 8, Appl1
3	1132	20.0	1084	US-08-455-543A-56	Sequence 56, Appl1
4	1132	20.0	1084	US-08-223-305C-56	Sequence 56, Appl1
5	1131.5	20.0	1103	US-08-455-543A-53	Sequence 53, Appl1
6	1131.5	20.0	1103	US-08-223-305C-53	Sequence 53, Appl1
7	1125.5	19.9	1079	US-08-455-543A-55	Sequence 55, Appl1
8	1125.5	19.9	1079	US-08-223-305C-55	Sequence 55, Appl1
9	1122.5	19.8	1091	US-07-745-206A-25	Sequence 25, Appl1
10	1122.5	19.8	1091	US-08-455-543A-52	Sequence 52, Appl1
11	1122.5	19.8	1091	US-08-223-305C-52	Sequence 52, Appl1
12	1122.5	19.8	1091	US-08-311-363-25	Sequence 25, Appl1
13	1118.5	19.7	1091	US-08-713-118-4	Sequence 4, Appl1
14	1118.5	19.7	1091	US-08-452-007-4	Sequence 4, Appl1
15	1116	19.7	1086	US-08-455-543A-54	Sequence 54, Appl1
16	1116	19.7	1086	US-08-223-305C-54	Sequence 54, Appl1
17	1080.5	19.1	1086	5386025-8	Patient No. 5386025
18	701	12.4	508	US-08-435-675B-6	Sequence 6, Appl1
19	145.5	2.6	946	US-09-074-579-3	Sequence 3, Appl1
20	145.5	2.6	946	US-09-388-774-3	Sequence 3, Appl1
21	141.5	2.5	942	US-09-074-579-1	Sequence 1, Appl1
22	141.5	2.5	942	US-09-388-774-1	Sequence 1, Appl1
23	135.5	2.4	885	US-09-074-579-5	Sequence 5, Appl1
24	135.5	2.4	885	US-09-388-774-5	Sequence 5, Appl1
25	134	2.4	3135	US-08-323-170B-2	Sequence 2, Appl1
26	134	2.4	3135	US-08-954-441-2	Sequence 2, Appl1
27	131.5	2.3	911	US-09-074-579-4	Sequence 4, Appl1

28	131.5	2.3	911	US-09-388-774-4	Sequence 4, Appl1
29	127	2.2	2366	US-08-480-604A-10	Sequence 10, Appl1
30	127	2.2	2366	US-08-405-496A-10	Sequence 10, Appl1
31	127	2.2	2366	US-08-915-136-10	Sequence 10, Appl1
32	126.5	2.2	766	US-08-951-648-2	Sequence 2, Appl1
33	126.5	2.2	766	US-09-174-437-2	Sequence 2, Appl1
34	126.5	2.2	803	US-08-951-648-4	Sequence 4, Appl1
35	126.5	2.2	803	US-09-174-437-4	Sequence 4, Appl1
36	125.5	2.2	779	US-08-951-648-6	Sequence 6, Appl1
37	125.5	2.2	779	US-09-174-437-6	Sequence 6, Appl1
38	117	2.1	906	US-08-094-889-1	Sequence 1, Appl1
39	115.5	2.0	869	US-08-483-101-15	Sequence 15, Appl1
40	115.5	2.0	2710	US-08-480-604A-6	Sequence 6, Appl1
41	115.5	2.0	2710	US-08-405-496A-6	Sequence 6, Appl1
42	115.5	2.0	2710	US-08-915-136-6	Sequence 6, Appl1
43	114	2.0	2257	US-08-611-107-10	Sequence 10, Appl1
44	114	2.0	2257	US-08-422-560A-10	Sequence 10, Appl1
45	114	2.0	2257	US-08-468-793-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-08-435-675B-5
; Sequence 5, Application US/08435675B
; Patent No. 5710250
; GENERAL INFORMATION:
; APPLICANT: Ellis, Steven Bradley
; APPLICANT: Williams, Mark E.
; APPLICANT: Harpold, Michael Miller
; APPLICANT: Schwardt, Arnold
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,675B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,083
; FILING DATE: 28-SEP-1994
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 08-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

FRAGMENT TYPE: Internal
US-08-435-675B-5

Query Match 20.3%: Score 1148.5; DB 1; Length 1106;
Best Local Similarity 28.5%: Pred. No. 1.5e-101;
Matches 320; Conservative 234; Mismatches 440; Indels 129; Gaps 39;

33 SEQOIPPLV-VKLMASAFGEIKSIKAKYSGSOLLQKKYKEKEDVAIEIDLOGLVKKL 91
DB 25 SEPPPSAVTISWVDKMOEDLVTLAKTASGVNQLVDIYEKIODLYTVEPNNAQLVEIA 84
92 AKNMEEMFKKSEAVRRLVEAAEAHLKHEPDADL---OYEFNAVLINERDKGNFLEL 148
DB 85 ANDIEKLLSNRSKALVRLALEAEKYQAHHQWREDFASNEVYVYNAK--DDLPKKNDESP 142
94 GKEFT--LAPNDHFNNLPVYNISLDVQVPTNKNKDPALVNGVYSESINKYFVNFDD 206
DB 143 GSQRIKPVFIDANFRROVSYOHAHVHPTDIYEGSTIVLNLNMTSALDDVFKKRNRED 202
94 PELINQVFGSAKGFPROYPGIKMEPDE---NGVIAFDCKNRKRYIOGATSPKDVYTLVDV 263
DB 203 PSLINQVFGSATGLARYTPASPVNDNSRTPKNKIDLYVRRPYIDGAASPDMLTLVDV 262
94 SCSMKGLRLTIKQTVSSILDTLGDDEFNIIAYNEELHYVEPCLNGTLVQADRTNKEHF 323
DB 263 SCSVSGTLKLRISVSEMLETLSDDDFVNASFSNADVS-CFQ-HLVQANVRNKKVYL 320
94 REHLDKLPKAGIGMDIALNEAFNIIISDENHGGSGICQALMLITDGAVDYDTIFAKY 383
DB 324 KQAVNNITAKGIDTYDKGFSFAEQLNANVSRA--CKIIMLFDFGGEERAQELFAKY 378
384 NMPDRKVRIFTLYIGREAFADNLKMMACANKGFETIOTSLADVOENMEYLVHLSRPKY 443
DB 379 N-KDKKVRFTSVQOHNDRCPIOMACENKGYEIPSGAIRNTQBYLDVLCRPVY 437
94 I--DOEHVDVMTYAVIYDSTLTDGCPVMTVAMPVFS---KQNETRSKG-ILLGVGST 496
DB 438 LAGDKRAKQVQMTNVYLDAL---ELG--LVITGTLPEVNTGQFENKTNLKQDILIGVMCV 492
94 DVPVVELKTIPTKYKLGINGVAFATNNQYILTHPELRL-----LYEGSKRRKRPYNS 550
DB 493 DVSLEDIRKLRPFTLCPRGYFAIDPNCGYVLLHPLOKPRIGVGIPITNLKRRRPNVON 552
94 VDLSEVEMEDRDV---LRNANVRKTKG--FSMEVK---KTVDSKGRVLVMT 595
DB 553 PKSOEPVTLDELDALENDIKYEIRNKMDGSEGEFTFTLVKSODERKIDIGNRI----- 608
94 NDYVYTDIKGTPFSLGVALSRGHGYFFRGVNTIEGLHLEHPVSLADEW----- 647
DB 609 -YVWTVPVGTDYSSIALVLPYISFYIYIKAK--IETITQARYSEFTLKPDNFEESGYFL 664
94 ---SYCNDTDLHEHRLHLSOLEIKLYLKKEP--LQCKKELLQEVLFDA-VVSAPLEAW 702
DB 665 APRDYC-SDLKSDNTEFLNFEINRKTPTNNSCNDLNRVLLDAGFTNELVQNVW 723
703 TSLALNKSSENSDKGEVAFAGTRGSLRNLFPVGAQLTNOFLKAGDKENIFNADHPFL 762
DB 724 S-----KQNKTKGVKAREVYTDGSTRYP-----KRGEMQWQENPEYEDS 765
94 WYRAAEQIPGSEVYSTIP--STGPNVNSNVVTASTISQLDERKSPVVAAGIOMKLEF 820
DB 766 FYKRLSDN--DNVYTPAFYFNKSGGAVESGIMSKAVEIYIOGKLKPAVVGKIDVNS 823
94 FQKRWTAASRQASLDGCSISCDDETVNCLYIDNNGFIVS--EDYT-QTDDFGGEIEG 877
DB 824 WLENTTKTSIRPCAGPVCDCKRNSDVMDCYLLDGGFLMANHDYTNQIRFGCEIDP 883
94 AVNNKLLTMGSEKRTILYDQAMCRANKESSDGAHGLDLPY-----NAFSAVWK 927
DB 884 SLMRLLVNIISVAFNKSVDYQSVCEPGAAPKGA--GHSAYVPSIADIIQITQWMTAAAM 942
94 IMTELVLFLVEF---NLCSMWHSDMTAKAOKLQTLPECDTEYPAFVSERTIKETGTNI 983

DB 943 SLIQOFLSLTFPRLLLEADMEDDPTASMSK-----QSCITEQFOYFFDNDKSPSGVL 997
94 ACEDCKSVIVIOQIPSSNLFPMVYVDS--SCICESVAPITMAPLEIRYNSLKCERKAK 1041
DB 998 DGCNCSRIHVEKLMNTNLIFFIMVESKGTCPDPT--RLIOAEQTSDEPDCDVKOPR 1054
94 IRRRPESCHGFHEENARECGA---PSLOA---QVLLLL 1076
DB 1055 YKRGPDVCFDNNVLEDTYDCCGVSGLNPSLMSITIGIQFVLMH 1097

RESULT 2

US-08-336-257A-8
Sequence 8, Application us/08336257A
Patent No. 5726035

GENERAL INFORMATION:

APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,257A
FILING DATE: 07-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 54898

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 238-0999

TELEFAX: (619) 238-0062

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

US-08-336-257A-8

Query Match 20.3%: Score 1148.5; DB 1; Length 1106;
Best Local Similarity 28.5%: Pred. No. 1.5e-101;
Matches 320; Conservative 235; Mismatches 439; Indels 129; Gaps 39;

33 SEQOIPPLV-VKLMASAFGEIKSIKAKYSGSOLLQKKYKEKEDVAIEIDLOGLVKKL 91
DB 25 SEPPPSAVTISWVDKMOEDLVTLAKTASGVNQLVDIYEKIODLYTVEPNNAQLVEIA 84
92 AKNMEEMFKKSEAVRRLVEAAEAHLKHEPDADL---OYEFNAVLINERDKGNFLEL 148
DB 85 ANDIEKLLSNRSKALVRLALEAEKYQAHHQWREDFASNEVYVYNAK--DDLPKKNDESP 142
94 GKEFT--LAPNDHFNNLPVYNISLDVQVPTNKNKDPALVNGVYSESINKYFVNFDD 206
DB 143 GSQRIKPVFIDANFRROVSYOHAHVHPTDIYEGSTIVLNLNMTSALDDVFKKRNRED 202

207 PSLIMQYGSAGKGFROYPGIKMEPDE---NGVIAFDRCNRKRYIOAASPQVYLVDV 263
203 PSLIMQYGSAGKGFROYPGIKMEPDE---NGVIAFDRCNRKRYIOAASPQVYLVDV 262
264 SGSMKGLRLTAKOTVSSILDTLGDDEFNIJAYNEELHYEPCLNGTLVQADRNTKEHF 323
263 SGVSGTLKLTIRTSVSEMLETLDDEEVNVAFSNSNADVS-CFO-HLVQANVNRKVL 320
324 REHDKLFAKIGIMDLALNEAFNLSDPNHTGGSGISQAIMLTLDGAVDTYDTIPAKY 383
321 KDAVNNITAKGITYDKKGFSAFEDLLNYSNRAN-CNKLIMLEPTDGEERAOBIFAKY 378
384 NMPBRKVRIFTYLIGREAFADNLKMACANCFEOTISTLADVOENMEYHVSIPRV 443
379 N-KDKKAVVFETFSQOHNYDGRPIOMACENKGYETELPSIGALINIOEYLDVGRPRV 437
444 I-DOEHVVTETAVYIDSTLDGQPVLMVTYAMPFS---KONETESKG-ILGVTGT 496
438 LAGDKAKOVQWNTNLYDAL---ELG-LVITGTLPVFNTGOFENKTLNKLNLILGVNGV 492
497 DVPKELKLTIPKYLGHGAFAITNNGYILHPELRL-----LYEGKKRRKRPNTSS 550
493 DVSLEDITRLPRFTLCNGYFFAIDPNGYVLLHPNLQPKPIGVGIPINLKRPRPVON 552
551 -----VDLSEVEMEDRDV---LRNANVNRKTKG-PSMEYK---KTVDKGRFVLVMT 595
553 PKSQEPVTLDLDALENDIVEITNKKMIDGSEKTRTLVKSODEKIDGNRT----- 608
596 NDYVTTDKIGPFSLGVALSRGHGKYPFRGNVTIEGLHLEHPDVSIADEM----- 647
609 -YMTVPNGDYSLALVLPYTSFYIYIKAK--IEFTIQARYSETLKPDPNEESGYFL 664
648 ---SYCNVDLPHENHLSQLEAIKILYKKEP-LLOCKELIQEYLFNA-VYSAPLEAVW 702
665 APRDGC-SDLKPSPDNTEFLNFEFIDRTPNNPSCNTDLINRVLILAGFTNELVQWNV 723
703 TSLALNKSENSDKGEVAFGLTRGTSRLNLFVGAEOQLNODFLKAGKENTFNADHPL 762
724 S-----KQNKIKGVKAFVYTDGKITRYP-----KAGLNMWQENPETIEDS 765
763 WYRRAAEQIPGSFVYSIFP--STGPVNSNVTASTSIOLEDERKSPYVAAGIOMKLEF 820
766 FYKRSIDN--DNYVETAYFENKSGPGAVESGIMSKAVEIYIQGKLLPAVVGITIDVNS 823
821 FQKRFWTASROCASLDGCSISCDDEVNCTYILDNNGTILVS--EDYR-QTGDFPGEIEG 877
824 WIENFTKTSIDPCAGPYCDCKRNSDVMDCVILDDGFLMANHDYINQIGRPFGEIDP 883
878 AVMNKLTMGSPKRTITLVDYQAMCRANKESSDGAHGLDPRY-----NAFISAVKW 927
884 SLMRLLVSIYAFNKSTDYOSVCEPGAAPNOGA-GHRSATVPSTADILQIGWMTAAAM 942
928 IMTELVLFLVEF---NLCSWMHSDMTAKAKLQKOTLEPCDTEYPAVSERTIKETGTNI 983
943 SILOQFLSLIFEPRLLEAAMDEDDFTASMSK-----QSCITEQOQYIPFNDNSKSFSGVL 997
984 ACEDCSKSFVIOQIPSSNULFNVVDS--SCLCESVAPITMABIEIRYNESLCEKELKAK 1041
998 DCGNCSRIFFHEKELINTMLIFIMVESKGTCPCDT---RLILQAEQTSJXDPDCDWKQPR 1054
1042 IRRPESCHGFPHENARECGA---PSLQA---QTVLILL 1076
1055 YRKGPVDFCNNVLEDTYDCGVSGLNPSLWSIIGIFVLLWL 1097

APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

US-08-455-543A-56

Query Match 20.0%; Score 1132; DB 1; Length 1084;
Best Local Similarity 28.4%; Pred. No. 5,6e-100;
Matches 322; Conservative 235; Mismatches 457; Indels 118; Gaps 41;

QY 14 ASALLAAL-LYALAGDVRSQOIPLSV-VKUMASAFEGCEIKSTIAKSSGSOLOQKKX 71
DB 3 ACCLATLTTLFOSLTIIGSSSEPEPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYE 62
QY 72 EYKDVAIIEIDGLQVLKLAKNMEEMFHKSEAVRIVEAAEALHKEFDADL---QY 128

Db 63 KYODLYVEPPNAROLVETIARDEKLEKLSNRSKALVSLALBAEKVOAHQWREDFASNEV 122
 129 EYFNVLNENDKGNFLELKEFI---LAPNDHNNLPVINSLSDOVOPNNMYKKDAI 185
 Db 123 VYTNKK--DDIDPEPNDSQSRKPYFIEDANGR-QISTQAAVAHPIDYIEGSTIV 179
 186 VNGVWSESLKRVENDRDPRLIMQYFGSAKGFEPGPKWEPDE---NGVIAPDCR 242
 Db 180 LNELNMTSALDEVEFRKKNNEEDPSLLMOVFGSATGLARYPASPWNDRTRPKIDLYVR 239
 243 NRKRYTQAATSPKDVYLIVDVGSKKGLRLTIAKOTVSSIIDTLCDDDFENIAYNEELH 302
 Db 240 RRPVYIOGASPKDMLLIVDVSGSVSGLTLRLIRTSVSEMLETSDDDFVNVASFNSAQ 299
 303 YVEECLNGTLVQADRTNKEHREHDLKFAKGIGMLDIALNEAFNISLDPHNTGGSGS 362
 Db 300 DVS-CFO-HLVOANRRKKVYLKDAVNNITAKGITDYKKGFSFAEQLLNVNVSRRAN--CN 355
 363 QAIMLITDGAVDYDTJTFKATNMPDRKVRIFTYILIGREAPADNLKMAKANKGFEFTOIS 422
 Db 356 KIIMLFTDGGSEBAGOEIENKYN-KDKKVRVRFSGVGHNERGPIOMKACENKGYEIEP 414
 423 TLADVOENMEYHLVLSRPKYI--DQEHVYVTEAYIDSTLTDDGCVLMTTVAAPVS- 479
 Db 415 SIGAIRITQOYLDVGLRPPVLAGKAKQOMTVYLDAL--ELG--LVITGTLPVENI 469
 480 ---KONETRSKG-ILGVVGTDPVYKELKTIPYKLGIGHYAFATNNGYILTHPELRL 535
 Db 470 TGOEENKTNLKNOLLGAGVDSLEDTKRLPRTLCPPNYRVIDPNGVYLHPNLO- 528
 536 LYEBGKKRRKNVSSVDLSEVEDRDOV-LRNAVNRKTGK--FSMEVK---KTYDKG 588
 Db 529 --PKNPSQOE--VLDPLDALENDIKVEIRNMKIDGSESEKFRILYKODEYIDKG 584
 589 KRVLVMTNDIYITIKGTPESLVALSRGCKYFPRGAVNTIEEGIHLEHDPVSLADEM- 647
 Db 585 NRT-----YMTVPNGDYSIALVLPY-YSFYIYIKAK--LEETITQARVSETLKPDME 635
 648 -----SYCNMDLPEHRHLSOLEAIKLYLKGEP-LLOCDKELOVLPDA-VVS 695
 Db 636 ESGTFTAPRICH-DLKISNNTTEFLNENEFIDRKTPNPNNSCHADLNNVLLDAGTGN 694
 696 APIEAYMTSLALNKSENSDKCEVAFLGTRTGLSRINLFGAEOLTNODFLKAGDENIF 755
 Db 695 ELVGNWS-----KQKNIKGVKARFVYTDGITRVYP-----KEAGENQEN 736
 756 NADHPLMYRRAAOITGSGFYSTPF--STGPVKSNNVYTAISTIQLLDEKRSPPVAAG 813
 Db 737 PETEDEFYKRSIDN--DNVYFTAPYFNKSGPAGVESGIMVSKAVEITYIOGKLKPAVVG 794
 814 IOMLEFFORFMTASROCASLDCGKISCDDEFVNCYLIDNNGFILVS--EDYT-OTGD 870
 Db 795 IKIDVNSMIENFTSTIRDPACAGVCCCKRNSDVWCYIIDDGFFLMAHNDITNOIGR 854
 871 FEGEISGAVMKLLTWGSEFKRITLYVOAMCRANKESSDGAHGLDPY-----NA 920
 Db 855 FFGESIDSLMHLVNIISYVAFNKSYDVQVCEPAAAPROGA-GHRSAYVPSVADILQIGW 913
 921 FLGAVKIMTELVEFLVEF---NLCSMHSDMAKAKOKLQTEPCDTEPAVSEKTI 976
 Db 914 WATTAANSILOQFLSTLFFPLLEAVEMEDDFTASLSK-----QSCITTEOTQFFEDMS 968
 977 KETGNTIACEDCSKSFYIOQIPSSNLFVAVVDS--SCLCSEVADPTMAPIRIRNESLKC 1034
 Db 969 KSPGCVLDCGCGSRIFGKEKMTNLIPIWESKGTCPCDTRILLIOAQEOTSDEGR--PC 1025
 1035 ERLAOKIRRRPESCHGFPEENARECGAPSLQAT--VLLPLPLMLMPS 1084
 Db 1026 DMVQOPRYRKCPDYVCFDNNVLEDYTDGCGVSGLNPMLWYIIGIQFILLMLVVS 1077

US-08-223-305C-56
 ; Sequence 56, Application US/08223305C
 ; Patent No. 5851824
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/223,305C
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/482,384
 ; FILING DATE: 20-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US89/01408
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/176,899
 ; FILING DATE: 04-APR-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 52516 (P519739)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999
 ; TELEFAX: (619)238-0062
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1084 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-223-305C-56
 Query Match 20.0%; Score 1132; DB 2; Length 1084;
 Best Local Similarity 28.4%; Pred. No. 5.6e-100;
 Matches 322; Conservative 235; Mismatches 457; Indels 118; Gaps 41;

3 AGCLLALTLFLFQSLIGPSSSEPPSAVTIKSWDKMOEDVTLAKTASGVNQLVDIYE 62
QY 72 EYKDVATIEIDGLQVKKLAKNMEMFHKSEAVRLEAEALKEHPEADL---QY 128
DB 63 KIÖDLYTEPNNAQVLEJAAARDIEKLSNRKALVSLLEAKVQAALQWREDFASNEV 122
QY 129 EYFNAVLINERDKDNFLFLGKEFI---LAPDHFNNILPVNLSLSDVCPYNNKNDPAI 185
DB 123 VYNNK--DDDLPEKNDSRPSQRIKPVFIEDANRGR-QISYQHAVALIPTDIEESTIV 179
QY 186 VNGVYSESINKVYVDNEDRPSLIMQVFGSAKGFROYPGIKWEPDI---NGVIAFDGR 242
DB 180 INELMWTSLADEVFKKREDEPSLLMOVYGSATGLARYPASPWYDNRKTPKNDIDYDVR 239
QY 243 NKKWYIQAATSPKDVYIIVDVGSKMGLBLTAKOVSSILDTLGGDUPFNITAYEELH 302
DB 240 RRPWYIQAASPKDMLILDVDSGVSGLTKLIRTSVSMLEFLSDIDIVNVAFSNMQ 299
QY 303 YVEPLNGTLVQADRNTKHEFHEDKLEFAKIGMLDIALNEAFNLSDFNHTGQSICS 362
DB 300 DVS-CFQ-HLVQANRNKKVLKDAVANNITAKGTDYKKGSFAFEQLNKNYSRAN--CN 355
QY 363 QAIMLTGADVDTYDTIEAKYMPDKRYRIFYLLIGREAPADNKKWACANKGFTQIS 422
DB 356 KIMLFTOGGEERAOEIFKRYN-KDKKYVRFESVQOHNYERGPDIOMACENKGYEIP 414
QY 423 TLADVOENMEYHLISRRKYI--DOEHVYVTEAVIDSTLDDOGPYLMTYAMVFS- 479
DB 415 STGAIRINQYELDVAGRWVLAGDAKOVONTNYLDL---ELG--LVITGTLVFNVI 469
QY 480 ---KONETRSK--ILGVGTVDPVKEELKTIPIKYKLGIGYAFATNNGYIILPELRL 535
DB 470 TQGFENKTKLAKNOLIGVAGVDSLEDIKRLPRFLCNGYFALDPBGVYLHLNLO- 528
QY 536 LYEBEKKRRKPNYSVDLSEVEDEDDV-LNNAMVNRRTGK--FSMEVK---KTVDRG 588
DB 529 --PKNPKSQEP--VTLDFDALENDIKVEIRNKMIDGSEKTEFTYKKSODERYIDKG 584
QY 589 KRVLVMTNDYTTDIKGFPSLGSVALSRGHKGYFFRGNTIEGLHDLLEHPOVSLADEN- 647
DB 585 NRT-----YTWTPVNGTDYSLALVLT-YSFYYIKAK--LEETIQAARYSEILKPDNEE 635
QY 648 -----SYCNFDLHPEHRLHLSOLEAIKLYLKKEP-LLOCDREKLOEVLFDA-VYS 695
DB 636 ESGTYFIAPRODCN-DLAKSDNTEFLNENFIDRKTPNNSCANDLNRVLLDGFN 694
QY 696 ADIEAYWTSLSLANKSENSDKVEYALGTRTGLSRINLEFGAEQLTNNDPLKAGDKENIE 755
DB 695 ELVONWMS-----KOKNIKGVAKRFVVDGGITRYP-----KEAGEMWQEN 736
QY 756 NADHPPLMKRRAEOLPGSFVYSIFP--STGPVNSNVYTTASTISLDDERKSPVAAVG 813
DB 737 PETYDSEFYKRSILDN-DWYVETAPFNKSGGAVESGIMVSAVYIYQGLKLPAAVVG 794
QY 814 IOMKLEFFORKFMTASROCASLDKCSISCDDETVNVCYLIDNNGFLIVS--EDYT-QOTG 870
DB 795 IVIDNWSMTEINTKTSIRPCAGPCVCDCKRNSDVMDCVLLDGGFLMANHDDYIMQIGR 854
QY 871 FEGEIGAVMNLTMGSEKRTITLYDYQAMCRANKESSDGAHGLIDFY-----NA 920
DB 855 FEGEIDPSLMRHLVNIISYVAFKNSDYQSVCEBGAAPKQGA-GHRSAYPVSADIIQIGM 913
QY 921 FLISAVKMWTELVLFLVER---NLCSMWHSMTAKAQLKOTLEPCDIETPAFVSEKRI 976
DB 914 WATPAAMSLLOOFLSLTFPRLLLEAVEMEDDFTASLSK-----OSCTEQTQYFFDNDNS 968
QY 977 KETTGNIACEDCSKSFVIOIPSSNLFNVVVS--SCLESYAPITMAPLEIRYNSLKC 1034
DB 969 KFSFSGVLDCGNSRIFHSGKLANLNLIFIMVESKGTCPDTRILLIDAEOTSDGPN---PC 1025
QY 1035 ERLKAOKIRRPRESCHGFHPEENARECGAPSLQAOT--VLLPLPLMLUFS 1084
DB 1026 DAWKQBPYRKGDVCFDNNVLEDYTDGCGVSGLNPISLWIIIGIQLFLMLVS 1077

RESULT 5
US-08-455-543A-53
Sequence 53, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-7926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
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APPLICATION NUMBER: 08/223,305
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PRIORITY APPLICATION DATA:
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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-455-543A-53

Matches 323: Conservative 233: Mismatches 460: Indels 121: Gaps 41:

Oy 14 ASALLAAL-LYALGIVRSBOQIPLSV-VKLMAAFGEIKSIARYSGSOLLQKRYK 71
 3 AGCLLATLTLFQSLILIPSSSEPPSAVTIKSWVDKMQEEDLVTLAKTASGYNQGLVDIYE 62
 Oy 72 EYKDVAAIEEDIGLOLVKLLKNMEEMFHKKSEAVRLVEAAEHLKHEPDAL---OY 128
 63 KYODLYTEPPNARQLVEIARDEIKLNSRSKALVSLALEEKVQAQAHQWEDFASNEV 122
 Oy 129 EYFNAVLINERDKDGNFLELCKEFT--LAPNDHENLPLVNISLDYOVPTNMYKKDPAI 185
 123 VYVNAK--DLDPEKNDESPSQRRKPFIEDANRGR-QISQMAVAHIFPDYIGSTIV 179
 Oy 186 VNGVYSESLKVFVNDNRDPSLIWOYFGSAKGFEPQYGIKWEPE---NGVIAPDCR 242
 180 LNELMTSALDEVPFKKNEEDPSLLMOYFGSATGLARYYPASPMWVNDRTPRKIDLYOVR 239
 Oy 243 NRKWTQAATSPKDVYLVYVSGSKGLRLTAKOTVSSILDTLDDDFNTIAYNEELH 302
 240 RRPWYIOGASPKDMLLVYVSGSVSGLTLKLTITSVSEMETLSDDDFVNVAFSNSNAQ 299
 Oy 303 YVEPCLNGLVQADRTNKEHFREHDKLFARIGIMLIALNEAFNILSDPNHTGGSGICS 362
 300 DVS-CFO-HLVOANVRNKKVLDKAVNNITAKGITDYKKGFSAFQQLNINVSRRAN--CN 355
 Oy 363 QAIMLITDGAVDYDTIFAKYNNPDRKVRIFTYLIGREAPADNLKMAKANKGFFTOIS 422
 356 KIIMLFTDGGERAQOEIRNKYN-KKKYVRFVFSQGNHNERGIOMWACEKGGYYEIP 414
 Oy 423 TLADVOENVMEYLHVLSPKVI--DQEHVYVTEAYIDSTLDDGPPVLMATTAMPVS- 479
 415 SIGAIRITQYGLDYLVGHPVLAGKAKOVMTNYLDAL---ELG--LVITGTLPIVNI 469
 Oy 480 ---KONETRSKG-ILLGVTGDPVKELKTIPIYKLGIGHYAFATINNGYITLHPERL 535
 470 TGOEENKTNLKNQILIGWGVDSIEDIKRLPRFTLCPNGYIFIDPNGLVLLHNLQ- 528
 Oy 536 LYEGKKRRKRNYSVDLSEVEMEDRDV-LRNAMVNRKTK--FSMEVK---KTYDKG 588
 529 --PKNPKQEP--VTLDFLDALENDIKVEIRNMKIDGESGKPTRLVKSODEYIDKG 584
 Oy 589 KRVLVMTNDYITDIKTPESLVALSGHCKYFF-----RCGNVITIEBL- 633
 585 NRT-----YMTVPNGTDYSLALVLP-YSEYIKAKLEETITQARSKGKMGKSETLTK 637
 Oy 634 -HDLHPDVSADKSYCNTDLHPHRLSQLKAIKLYLKEP-LLOCDKLEIOEVFD 691
 638 PDNFEESGYTIARPDICN-DLKISDNTEFLNFEIDRKTTPNNPSCNADLNRVLID 696
 Oy 692 A-VVASPIEAAYTSLALNKSSENSDKGEVAFIAGTGTGLSRINLFYGAQOLTNODELAKAD 750
 697 AGFTNELVQNWMS-----KQKNIKGVARFVYVDCGITRYR-----KEAGE 738
 Oy 751 KENFNADHFLMYRRAAEQIPGSFYISIP--STGPVKNKSNVYTAISTOLDERSKAPV 808
 739 NMQENPETEYDSFYKRSIDN--DNVVFAPYFNKSGPAGVSGIWSKAVEIYIOGKILK 796
 Oy 809 VAAVGIQMKLEFFQKKEFWTASROCASLDGKCSISODDETVCYLIDNNGFIYVS--EDYT 866
 797 PAVYGIKIDVMSJIENTFKTISIRDPACAPVDCCKRNSDVMLCCVIIDDGFLIMAHNDYT 856
 Oy 857 NQIGRFGEIDPISLMRHLVNISYVAFNKSVDYQSVCEGAPKQGA-CHRSAYPSVADI 915
 919 ---NAFLSAVVMITELVLFVER---NLCSMMHSDMTAKAKLIKOTLECDIETPAFV 971
 916 LQIGMATTAAMSLIOQFLSLTGPRLLEAVEMEDDFTASLAK---QSCITEQOTYF 970
 Oy 972 SEPTIKETGYNIAECDSKSVIOQIPSSNLFMVVVS--SCLCESVAPITMAPIEIKYN 1029
 971 FDNDSKFSFSGVLDCGKNSRIFHGKELMNTNLIIFTVESKGTCPDTRILLIOAEOTSQPN 1030

Oy 1030 ESKCERLKAOKIRRRPESCHGFHPEENARECGAPSLQADT-VLLLLPLLLMFLS 1084
 1031 ---PCDMVKOPRRYRGPDVCCFDNNVLEDTYDCGVSGLNPSLWYIIGIOLFLLMLVS 1084

RESULT 10
 US-08-455-543A-52
 Sequence 52, Application US/08455543A
 Patent No. 5792846
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 TITLE OF INVENTION: METHODS
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1091 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-08-455-543A-52

Query Match 19.8%; Score 1122.5; DB 1; Length 1091;
Best Local Similarity 28.4%; Pred. No. 4.7e-99;
Matches 323; Conservative 233; Mismatches 460; Incls 121; Gaps 41;

QY 14 ASALLAAL-LYALAGDVRSQQIPLSY-VKLMSAFGEFKLSIAAKYSSQLLOKKK 71
DB 3 AGCLLATLTLTQSLIGPSSSEPPSAVTIKSWDKMQEEDLVTLAKYASGNOLVDIYE 62
QY 72 EYKQVAIEEIDQLQVYKLLAKNMEEFHKKSEAVRRLVEAAEHLKHEFDADL---QY 128
DB 63 KYQDLYTEPNNARQLVEIARADIKLSNSKALVALALEKQVAAHOMEDPASNEV 122
QY 129 EYPAVLINERDKGNFLELCKEFT--LAPNDHPNMLPVNISLSDVQVPTMYNKPDAI 185
DB 123 VYNNAK--DDIDPEKNDSEPGSQRIKPVFIEDANFGR-QISYQAAVHIPTDIYEGSTIV 179
QY 186 VNGVYMSLKKVFPVNDROPSLIMQYFGSAKGFROYPGIKMPEPD---NGVIAFDGR 242
DB 180 LNEIIMWTSLALDEVPFKNNEEPPSLIMQYFGSATGLARYPASPVWDCNRTPKIDLYDVR 239
QY 243 NRKWTQAATSPKDVVILVDVSGSMKGLRLTAKQTVSSIIDTLGDDIPEFNIIAYNEELH 302
DB 240 RRPWTIQGAAPKMDLILVDVSGSVGLTLKIRTSVSEMLETISDDIFVNVASFNSNAQ 299
QY 303 YVEPLNGLTVOADRTNKEHFREHLDKLFGANGIMDIALNEAFNILIDFNHTGOGSICS 362
DB 300 DVS-CFQ-HLVOANVRNKKVLKDAVNNTAKGITDYKKGFSFAEQLLNVNYSRAN-CN 355
QY 363 QAIMLITGADVITYTTIAKTNMPDKRYRIETYLIGREAPADNLKMAACANKGFFTOIS 422
DB 356 KIMLFTDGGEGRAQELINKNY-KDKKRVPRFVSQHNHERGPLOMIACEKKGYYEIP 414
QY 423 TLADQENVMEXLTVLSRPKYI--DOEHNVWTEAYIDSTLTDGQPVLMTVAPVPS- 479
DB 415 SIGARITQERLDVLRPMVLACGAQOVQNTNYLDL---ELG--LVITGTLPEVNI 469
QY 480 ---KONETRSKG-ILGVGTVDPVKELTKTIPKYLGIHGAFAITNGYILTHPELRL 535
DB 470 TGFENKTNLKNQILGVGADVSLIEDIKRLPRFTLCPNGYFAIDPVGYYLHPNLD- 528
QY 536 LYEECKRRKRRNYSVDLSEVEMEDRDV-LRNAMVNRKTKG--FSMIYK---KTVDKG 588
DB 529 --PKNPKSOEP--VTLDELALDELNDIVEIIRNMKIDGSGEKTERTYVKSODERYIDKG 584
QY 589 KRVLMTNDYTYTDIKGTPFSIGVALSRGHGKYPF-----RGNVITEEGL- 633
DB 585 NRT-----YWTVPVNGTDYSIALVLPY-YSFYIYIKALEETITQARSKKGMKSEITLK 637
QY 634 -HDLHPDVSLADEWSYCNLDLHPEHRLSOLEAIKLYLKGEP-LLAQCKELIOEVLEFD 691
DB 638 PDNFEEESGYTFIAPDYCN-DLKISDNNTFELFNNEFIDRKTPNPNPCSNADLIRVLDD 696
QY 692 A-VVSAPLEAVYTSIALKKSNSDKGVAVPLGTGTSRLTFLFGAQLTQODLLKAGD 750
DB 697 AGFTNELVQONWS-----KQKNINGVAKRPFVVTGGITRYV-----KEAPE 738
QY 751 KENIFNADHPFLMYRRAEQIPGSFVYSIPF--STGPNKSNVYVASTNSIOLDEKSPV 808
DB 739 NMQENPETEYDSFYKRSIDN--DNVYFAPYFNKSGPGAYESGIAVSKAVELYIOGKLK 796
QY 809 VAAVGIOKLEFFORFETASRQCSALDQKCSISCDDETVCNCLIDNNGFIVLS--EDYT 866
DB 797 PAVYGIKIDVNSMIENFTKTSIRDCACAPVCCKRNSDVCVILDDJGFFLLAMHNDYT 856
QY 867 -QTGFPEEIGCAVYNNKLLTMSFKRITLYDQAMCRANKESDGAHGLIDPY----- 918
DB 857 NOIGFFFEIDPISLMRHLVNIISVAFNKSYDQVSCGCAAPKGA-GHRSAYVPSVADI 915
QY 919 ---NAFISAVKIMTELVLVEF---NLCSWHSMDMTAKQKQLTLEPDETEYPAFV 971

DB 916 LQIGWMTAAASIIQQFLLSLTFPRLLAEVEMEDDFTASLSK-----QSCITEQTYF 970
QY 972 SEBTIKETGNIACEDCSKSEFVYIQIIPSSNLEPMVVD--SCLCESVAPITMAPIEIRN 1029
DB 971 FNDSSFSFGVLDCCGNSRIFGEEKLMNTNLFIINVESKGTCPCDRLILOAEQTSDCFN 1030
QY 1030 ESILCKERLAKQIRRRPECHGFHPEENARECGGASLQAT--VLLLPILLMLFS 1084
DB 1031 ---PCDMVAKQPRKGPVDCFDNNVLEDYTDGCGVSGLNPISLWYIIIGIOPILLMLVS 1084

RESULT 11
US-08-223-305C-52
Sequence 52, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 19.8% Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4% Pred. No. 4,7e-99;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;

14 ASALLAAL-LYALGADVRSQQIPLSV-VKLMSAFGGEIKSIANKYSSQLQKKYK 71
3 AGCLIALTLTLFGSLILGSPSEEPSPASVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
72 EYKDVAAIEELIDGQLYKLLAKNMEEFMHKKSEAVRRLVEAEHAKLHEPDAL---QY 128
63 KYODLYVEPPNNAKOLVYIAARDEIKLSNRSKALVSLALEKAKQAHAHQWEDPASNEV 122
129 EYFNAVLINERDKDNLELGKEFI---LAPNDHFNLPVNISLSDVOPTNMYNKKDPAI 185
123 VYVNAK---DDLDPKNDSEPSQRIKPFIEDANGR-QISYQNAVAHIPIIDYEGSTIV 179
186 VNGYVSSSLKKYVVDNDPRLIMQYFGSAKGFROYPGIKWEPDE---NGVIAFCR 242
180 LNELNMTSALDEVERKKNKEEDPSLIMQVFGSATGLARYYPASPVWDNSRTPKIDLYDVR 239
243 NRKVTIQATSPKDVILIVDSGSMKGLRTIAKOTVSSILDTLGDDEFNIIAYNEELH 302
240 RRPVYIGAAKSPKMLILVDSGVSGLTKLIRTSVSEMLETSLDDDFVYVNASNSMAQ 299
303 YVEPCLNCTLVQADRTNKEHREHLDKLEAKGIMLALNEAFNILSDFNHTGGSGICS 362
300 DVS-CFO-HLVOAVNRNKKVLDAVNNTAKITDYKKGFSFAEQLLNVYSRAN-CN 355
363 QAILIITDGAANDTDTYFAKNMPDRKVRITTYLIGREAAADNLKMAKANGKGFOTIS 422
356 KIMLFTDGGGERAOEIFNKN-KDKKAVREFSVOGHNYRGPLOMAKCEKGGYVIRP 414
423 TLADVENMVEYLVLSHPKYI---DOEHVMTVEAYIDSTLDDGAPVLTMTVAAPVES- 479
415 SIGAIRINTQYLDVIGRPVYLADKAKQVOTVNYLDAL---ELG-LVITIGLIPVNI 469
480 ---KONETRSGK-ILGAVGTDVPVKELTKTPYKKGIGHYAPAITNGYIILHPELRL 535
470 TGOENKRNILNQLILGVGVDLEIDIKRLTPRETLCPNGYFEAIDNGVYLLHPNLQ- 528
536 LYEGRKKRKRKNYSVDLSEVEMEDRDV-LRNAMVNRKTKG--FSMEVK---KTVDKG 588
529 --PNPNSQEP-VTLDFLDALELNDIKVELIRNMKIIDEGSEKTFRTLKVSQDERYIDKG 584
589 KRVLMNTDYYTDIKGTPESIGVALSRGHGKYF-----RGNVTIEEGL- 633
585 NRT-----YMTFVNGTIDYSLALVLP-YSFYIKAKLEETIQARSKKKMKMDSFLK 637
634 -HDLHPDVSLADEMSTCNDLAPRHRHLSQLEAIKLYLKEKP-LLOCDKELIOEVLFD 691
638 PDNFEESGYTFIAPRDYCN-DLKISDNNTFELNPFNEFIDRKTNNPSCNADLIRVYLD 696
692 A-VVSAPIEAVWTSIALNKSNSDKGEVAVFLGRTGSRINLVEGAQQLNODFLAKGD 750
697 AGFTNELVQNTWS-----KKNNIKGVAKARFVVDGCTIRYP-----KEAGE 738
751 KENIFNADHFLMYRAAEQIPGSEFVSIFP--STGPVKNKNVYASTSIOLDERKSPV 808
739 NMGNPEPEYEDSFYKRLSDN--DNVYTFAPYFNKSGPGAYSGIMVSAVAEYIYQKILK 796
809 VAAVGIOMKLEEFQKRFKWTASRQCASLDGKCSISCDDETVNICYLIDNNGFLVVS--EDYT 866
797 PAVYAGIKIDVMSIENFTKTSIRDPACAPVDCRKNSDVMDCVILDDGFLIMNHDDYT 856
867 -QTDVFGELIEGAVMNKLLTMGSEFKRITLYQAMCRANKSESSDGAHGLDPPY----- 918

DB 857 NOIGRFGELIDPSLMRHLVNISVYAFNKSVDYQSVCEPGAAPKOGA-CHRSAYVPSVADI 915
QY 919 --NAFLSAVKWIMTELVLVEEF-----NLCSWMHSDMTAKAKLQTLLEPCDREYPAFV 971
DB 916 LQIGMMATRAAMSILOQLLSITFFRLEAVEMEDDFTASLSK-----QSCITFGQIYF 970
QY 972 SERTIKETTGNIACEDSKSFYIQIIPSSNLFMVVVS--SCLESVAPITMAPIEIRYN 1029
DB 971 FDNDSKSFSGVLDCGNCGRIFGEIKLMTNLIFFIWESEKGTCPCDTRLIIQAEOQSDGPN 1030
QY 1030 ESLKCEKRLKAKIRRRPSCCHGFHEENARECGAPSLQAQT--VLLLLPILIMLFS 1084
DB 1031 --PCDMVKQPRYKRPVPCFDNNVLEDTYDGGVSGLNPISLWYIIGIQFLILWLVS 1084

RESULT 12
US-08-311-363-25
Sequence 25, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: Human Calcium Channel Compositions and
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25
Query Match 19.8% Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4% Pred. No. 4,7e-99;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;
14 ASALLAAL-LYALGADVRSQQIPLSV-VKLMSAFGGEIKSIANKYSSQLQKKYK 71
3 AGCLIALTLTLFGSLILGSPSEEPSPASVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
72 EYKDVAAIEELIDGQLYKLLAKNMEEFMHKKSEAVRRLVEAEHAKLHEPDAL---QY 128

Db 63 KYODLYTEVPNNARQOLVETIARDIEKLLSNRSKALVSLALEAKVOAHQWREDFASNEV 122
QY 129 EYFNNAVLINEBKDGNFLELGEFT---LAPNDHFNNLVNISSLVQVPTNMYNKDPAL 185
Db 123 VYNNAK--DOLPEKNDSEPGSORIKPVEIEDANFGR-QISYOAHAHVHPTDIYEGSTIV 179
QY 186 VNGVYSESLNKVFVNDNFDRPSLIWQYFGSAKGFROYPGIKWEDE---NGVIAFDOR 242
Db 180 LNEIWNMTSALDEYFKKRNREDEPSLIWQYFGSAGTLARYPASPVWVNSRTPNKIDLYDR 239
QY 243 NRKWTIOATSPKDVVILVNVSGSMKGLRTLTAKOTVSSILDTGDDDFENIAYNEELH 302
Db 240 RRPVYIOGAASPKDMLILVNVSGVSGTLKLRISVSEMLETISDDDFVNAVASFNSMQ 299
QY 303 YVEPCLNGTLVQADRTNKEHREHLDKLEPAKIGMDILNEAFNITLSDPNHTGOGSICS 362
Db 300 DVS-CFQ-HLVQANVRKVKLVDAVNNITAKGTLTDYKKGFSFAFEOQLNMYNSRAN--CN 355
QY 363 QAIMLITDGAVDYDTIFAKYNNMPDRKVRIFTYLIGREAAFDNLKMACANKGFTQIS 422
Db 356 KIMLFTDGEERAQEIFNKYN-KDKKVYVFRFVSGOHNYERGPIDWACENKGYIYEIP 414
QY 423 TLADVOENMEYLHVLSPKVI--DOEHNVTEAYIDSTLTDGQPVYLTMTVAMFVS- 479
Db 415 SIGAIRINQOETLDVLRGMVLAGRAKQVMTNVDLAL---ELG-LVITGTLVFN 469
QY 480 ---KONERSKG-ILLGVGTVPYKELIKTIPKYLGHGAFAITNNGYIITHEBL 555
Db 470 TGOFEKRTYKQOLILGVGVSVSLEDIKRLTPRFILCPNGYFAIDPBGYVLLHFNLO- 528
QY 536 LVEEGKRRKPKVSVSDVSEVEMEDRDY-LRNAVNRKTGK--FSMEYK---KIVDVG 588
Db 529 --PKNPKSEPP--VITDFDALENDIKVEIRKMKIDGESGKTEFTLVKSDERIDY 584
QY 589 KRVLVMTNDYVYTDIKGTPSLGVALSRGHGYFF-----RGVYIEGL- 633
Db 585 NRT-----YTWTPVNGTDYSLALVPT-YSPFYIKAKLEETITQARSKKGMKDESLK 637
QY 634 -HDLHPDVSLADENSYCTDLHPEHRHLSOLEAIKLYLKGKPP-LLJCDKELIQEVL 691
Db 638 PNFEEGTYFTIAPRDYCN-DKISDNNTFELNFEFTIDRKTPNPNPSONADINRVLLD 696
QY 692 A--VVSAPIRAYTSLALNKSSENSDKGEVAFLGTGTGLRINLFVGAEDQTLNDQFLKAG 750
Db 697 AFTNELVQVNS-----KOKNIKGVKARFVYVTDGCTITRVF-----KEAGE 738
QY 751 KENIFNADHFLMYRRARAOIPGSEFYISIPF--STGPRVKSNNVYVASTSIQLDERKSPV 808
Db 739 MNQENPEYEDSFYKRSIDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLK 796
QY 809 VAAVGIOMKLEFFORKFWTASROCASLDGKCSISCDDEFVNCYLIDNGFIIVS--EDYT 866
Db 797 PAVVGKIDVNSMIENFTKTSIRDCPAGVCCCKRNSDVMDCVILIDGDFLLMANHNDYT 856
QY 867 -OTGDFEGIEGAVNNKLTITMGSKRITLYDQAMCRANKESDGAHGLIDP----- 918
Db 857 NOIGRFFGIDSLMHLNINISVYAFNKSVDYQSCPEGAAPKQGA-GHRSAPVPSVADI 915
QY 919 ---NAFLSAVKIMTELVLVEF---NLCSSMWSMDTAKAOKLCTLEPCDTEPAFV 971
Db 916 LQIGMMATTAASIIQOFLSLTLFPRLLAVEMEDDDFTASLSK-----QSCITDEQYF 970
QY 972 SERTIKETTGNIACEDCSSEYVIOQIPSSNLEMVNVDS--SCLCESVAPITMAPIEIRYN 1029
Db 971 FNDSEISFSGVLDGNCSCSIFHGEKLMNTNLFIWESKGTCPDPCDFLLIOAEOISDGP 1030
QY 1030 ESUKCERLAKOIRRRPESCHGFHPEENARECGAPSLAQOT--VTLILPILIMLS 1084
Db 1031 ---PCDMVQOPRIKRGPDVCFDNNVLEDYTDGCGVSGLANPSLMTYIGIOFLMLIVS 1084

RESULT 13
US-08-713-118-4

Sequence 4: Application US/08713118
Patent No. 6040436
GENERAL INFORMATION:
APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
NUMBER OF INVENTION: CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,118
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4

Query Match 19.7%; Score 1118.5; DB 3; Length 1091;
Best local similarity 28.4%; Pred. No. 1.2e-98;
Matches 323; Conservative 222; Mismatches 461; Indels 121; Gaps 41;

QY 14 ASALLAAL-LVYALGDVRSQOIPLSV-VKLWASFGGEIKSIAKYSGLLOKRYK 71
Db 3 AGCLALTLFLFSLIGPSSEPPPSAVITKSMVDMQMDLVTLAKTAGVNOVDIYE 62
QY 72 EYEKDAIEIDIGLOLYKTKAKNMEEMFKKSEAVRRLVAAEBAHLKHEFDADL---QY 128
Db 63 KYODLYTEVPNNARQOLVETIARDIEKLLSNRSKALVSLALEAKVOAHQWREDFASNEV 122
QY 129 EYFNNAVLINEBKDGNFLELGEFT---LAPNDHFNNLVNISSLVQVPTNMYNKDPAL 185
Db 123 VYNNAK--DOLPEKNDSEPGSORIKPVEIEDANFGR-QISYOAHAHVHPTDIYEGSTIV 179
QY 186 VNGVYSESLNKVFVNDNFDRPSLIWQYFGSAGGFROYPGIKWEDE---NGVIAFDOR 242
Db 180 LNEIWNMTSALDEYFKKRNREDEPSLIWQYFGSAGTLARYPASPVWVNSRTPNKIDLYDR 239
QY 243 NRKWTIOATSPKDVVILVNVSGSMKGLRTLTAKOTVSSILDTGDDDFENIAYNEELH 302
Db 240 RRPVYIOGAASPKDMLILVNVSGVSGTLKLRISVSEMLETISDDDFVNAVASFNSMQ 299
QY 303 YVEPCLNGTLVQADRTNKEHREHLDKLEPAKIGMDILNEAFNITLSDPNHTGOGSICS 362
Db 300 DVS-CFQ-HLVQANVRKVKLVDAVNNITAKGTLTDYKKGFSFAFEOQLNMYNSRAN--CN 355
QY 363 QAIMLITDGAVDYDTIFAKYNNMPDRKVRIFTYLIGREAAFDNLKMACANKGFTQIS 422
Db 356 KIMLFTDGEERAQEIFNKYN-KDKKVYVFRFVSGOHNYERGPIDWACENKGYIYEIP 414


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Db 580 NRT-----YWTVPVNGTDYSLALVLPY-YSEYYIKAKLEETITQARSKKGMKDETLK 632
QY 634 -HDLHPVSLADEWSYCNTOHLPEHRHLSOLEAIKLYLKKEP-LLOODKELIOEVLFD 691
Db 633 PDNFEESGYTIFAPRDYCN-DIKISDNNTTEFLNENETDRKTPNPNPCNADLINRVLLD 691
QY 692 A-VVSAPIEAYWTSIALNKSENSDKGEVAFGLGTRTGLSRINLFPVGAQOLTNODEFLKAGD 750
Db 692 AGFTNELQYNVWS-----KQKNIGVAKARFVVTGGITRVYP-----KEAGE 733
QY 751 KENTFNADHFLPMTARRAEQIIPGSFYISIPF-STGPVKNKSNVTASTSIQLLDERKSPV 808
Db 734 NMOENPETYEDSFYKRSLDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLK 791
QY 809 VAAVGIOKLEFFORKFWTASROCASLDGKCSISCDDETVNCTYLDNNGFILVS--EDYT 866
Db 792 PAVVGIKIDVMSWLENFTKTSIRDPACAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYT 851
QY 867 -QTGDFEGEIGAVVNKLLTNGSFKRITLYDYQAMCRANKESSDGAHGLDLPY----- 918
Db 852 NQIGHFEGEIDPISLMRHLVNISVYAFNKSVDYQSVCEPGAAPKGA-GHRSAYVPSVADI 910
QY 919 ---NAFLSAVMIMTELVLFLVERF---NLCSMWHSMTAKAKQKQTLBPCDTEYPAFV 971
Db 911 LQIGWMATAAAMSILOQFLSLTFEPRLLAEVEMEDDFTASLSK-----QSCITEQOTQYF 965
QY 972 SERTIKETTGNIACEDSKSFVIOIPSSNLFMVVYVDS--SCICESVAPITMAPIEIRYN 1029
Db 966 FDNDSKSFSSGLDCGNCSCRIFHGEKLMNTNLIETIVESKGTCPCDTRLILQAEQTSDDPN 1025
QY 1030 ESLCERLKAQKIRRRPESCHGFHEENARECGAPSLQAQT--VLLLLPILLMLFS 1084
Db 1026 --PCDMVKQPRYRKGPVPCFNNVLEDTYDCGVSGLNPISLWYIIGIQFILLMLVS 1079
```

Search completed: August 16, 2002, 22:19:12
Job time: 7667 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 20:21:55 ; Search time 11.02 Seconds
(without alignments)
1286.805 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667
Sequence: 1 MAGGSPRRASRGASALLAA.....SLQAQTVLLPLLLMLFSR 1085

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5524	97.5	1091	2 T30256	calcium channel al
2	1148.5	20.3	1106	1 CHRBA2	calcium channel pr
3	1122.5	19.8	1091	2 JH0565	calcium channel al
4	1114.5	19.7	1091	2 A44147	calcium channel pr
5	716.5	12.6	734	2 S44617	C50C3.11 protein -
6	561	9.9	1148	2 T18770	probable calcium c
7	203	3.6	1450	2 C86880	hypothetical prote
8	166.5	2.9	886	2 S54355	inter-alpha-trypsi
9	162.5	2.9	889	2 JC5576	inter-alpha-trypsi
10	160	2.8	570	2 AC2356	hypothetical prote
11	156.5	2.8	946	2 S54354	inter-alpha-trypsi
12	156.5	2.8	946	2 JC5575	inter-alpha-inhibi
13	154.5	2.7	946	1 IYH02	inter-alpha-trypsi
14	153	2.7	2166	2 G70163	hypothetical prote
15	152.5	2.7	914	2 JC5574	inter-alpha-trypsi
16	151.5	2.7	930	2 JX0368	inter-alpha-trypsi
17	146.5	2.6	1297	2 S39791	neurotoxin - Clost
18	140	2.5	1021	2 T15900	hypothetical prote
19	139.5	2.5	1302	1 JC6009	surface-located me
20	139	2.5	5005	2 F82884	hypothetical prote
21	138.5	2.4	1127	2 T88317	ORF MSY156 hypothe
22	138.5	2.4	1552	2 G86344	T22111.2 protein -
23	138.5	2.4	3724	2 T18427	hypothetical prote
24	138	2.4	436	2 E90261	hypothetical prote
25	138	2.4	1232	2 H91178	ATP-dependent exon
26	137.5	2.4	739	2 E97245	beta-lactamase cla
27	137.5	2.4	911	2 A39667	inter-alpha-trypsi
28	137	2.4	888	2 C90595	hypothetical prote
29	136.5	2.4	907	2 S54353	inter-alpha-trypsi

30	136	2.4	2401	2 T28676	rhodopy protein -
31	135	2.4	1440	2 T33813	hypothetical prote
32	134	2.4	876	2 G89952	DNA polymerase I l
33	134	2.4	3135	2 A48584	transmission block
34	132.5	2.3	435	2 F96939	TPR repeats contai
35	132.5	2.3	885	2 S30350	inter-alpha-trypsi
36	132.5	2.3	906	1 JN0607	alpha-catenin 1 -
37	132.5	2.3	932	2 JC5953	inter-alpha-inhibi
38	132.5	2.3	1088	1 P1XRP	inner layer protei
39	132	2.3	758	2 C96749	hypothetical prote
40	131.5	2.3	649	2 B71826	type II DNA modifi
41	131.5	2.3	676	2 T47637	hypothetical prote
42	131	2.3	448	2 C82936	signal recognition
43	131	2.3	1377	2 D90538	hypothetical prote
44	130.5	2.3	811	2 AB1980	two-component hydr
45	130.5	2.3	3351	2 T13812	lipophorin - fruit

ALIGNMENTS

RESULT 1
T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A>Title: Molecular diversity of the calcium channel alpha2delta subunit.
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <KLD>
A:Cross-references: EMBL:AV010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

Query Match	Best Local Similarity	Score	Pred. No.	Length
Matches 1064;	Conservative 2;	Mismatches 19;	Indels 6;	Gaps 1;
QY 1	MAGGSPRRASRGASALLAAALYALGDVRSQQIPLSVKIMASAFGEIKSIATKY 60			
DB 1	MAGGSPRRASRGASALLAAALYALGDVRSQQIPLSVKIMASAFGEIKSIATKY 60			
QY 61	SGSOLLQKKRYEKYKVDVAIEIDGLQVKKLAKMEEMFKKSAVRLVEAAFEALKH 120			
DB 61	SGSOLLQKKRYEKYKVDVAIEIDGLQVKKLAKMEEMFKKSAVRLVEAAFEALKH 120			
QY 121	EPFADLQYEFNVLINERKDGNEFLGKEFILAPDHNNLPVNSLSDVQPTMYN 180			
DB 121	EPFADLQYEFNVLINERKDGNEFLGKEFILAPDHNNLPVNSLSDVQPTMYN 180			
QY 181	KDAIVGVVWSLKNVFNDFRDSLIMQYFGSAKGFROYGKIWEDENGVIAPD 240			
DB 181	KDAIVGVVWSLKNVFNDFRDSLIMQYFGSAKGFROYGKIWEDENGVIAPD 240			
QY 241	CRRKWTIOAATSPKVDVILVDVSGSKGLRLTAKTVSSILDTLGDDEFNITIANEE 300			
DB 241	CRRKWTIOAATSPKVDVILVDVSGSKGLRLTAKTVSSILDTLGDDEFNITIANEE 300			
QY 301	LHVEPCLNGLTVOADRTNKEFHREHDKLPAFGIGMLDIALNEAFNILLSDFNHTGSGSI 360			
DB 301	LHVEPCLNGLTVOADRTNKEFHREHDKLPAFGIGMLDIALNEAFNILLSDFNHTGSGSI 360			
QY 361	CSOAIMLITDGAVDYDTIFAKYNWPKRVRIFTYILIGREAPADNKKMACANKGFFTO 420			
DB 361	CSOAIMLITDGAVDYDTIFAKYNWPKRVRIFTYILIGREAPADNKKMACANKGFFTO 420			
QY 421	ISTLADQENVMEYLAHLSRPKVIDGHDVVMVEAYIDST-----LTDDQGPVLMTTVA 474			


```
Db 766 FYKRSIDN--DNVYFAPYFNKSGPAGESGIMVSKAVEIYIOGKLLPAVVGKIDVNS 823
Qy 821 FQRKFTAROCASLDGKCSISODDETVNCYLIDNNGFLTVS--EDYF-QTGPFPEIEG 877
Db 824 WIENFTKTSIRPCAGPYVDCRNSVMDCVLIDDGFFLMAHNDYVNOIGRFEIDP 883
Qy 878 AVMNKLITMGSEKRLILYQAMCRANKESSDGAHGLDLPY-----NAFLSAVKW 927
Db 884 SLMRHLVNSVYAFNKSTYQVCEGAPAKOGA-GHRSAYPSTADLQIGMATAAAM 942
Qy 928 INTELVFLVER---NLCSMWHSMTAKAOKLKQTLPECDREYPAFVSERTIKETGTNI 983
Db 943 SILQFLSLTFEPRLLEADMEDDEDTASMSK-----QSCITFQTOYFEPNDKSPRSYVL 997
Qy 984 AEDCSKSVIOQIPSSNLFMYVDS--SCLESVAPITMAPLEIYIESLKCERLKAQK 1041
Db 998 DGCNCSRIHFVERKLMNTNLIFFIMVESKGTCPDPT---RLLIQAQTSIDGPPCDMVKOPR 1054
Qy 1042 IRRPESCHGFHEENARECGA---PSLQA---QTVLLLL 1076
Db 1055 YKKGPPVCHDNNVLEDTYDCGGVSGLNPSLWSTIGIQLPVLWL 1097

RESULT 3
JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JH0565
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellicelebl, G.; Ellis, S.B.;
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of a
A:Reference number: JH0564; MUID:92110010
A:Molecule type: mRNA
A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M76559; NID:9179761; PID:AAA51903.1; PID:9179762
A:Experimental source: basal ganglia
A:Note: several conflicts are found between GenBank submission, authors' translation in
C:Comment: This protein is a subunit of the voltage dependent calcium channel.
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domains: signal sequence #status predicted <Sig>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
F:32, 268, 326, 539, 635, 1087/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
F:91, 142, 250, 623, 817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
F:92, 136, 184, 324, 348, 475, 585, 594, 682, 769, 812, 883, 973, 986/Binding site: carb
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 19.8%; Score 1122.5; DB 2; Length 1091;
Best Local Similarity 28.4%; Pred. No. 7, 1e-62;
Matches 323; Conservative 233; Mismatches 460; Indels 121; Gaps 41;

Qy 14 AASLLAAL-LVAALGVVRSQQIPLSY-VKIMASAFGEIKSIAXKSGSOLLQKKY 71
Db 3 AACLALTLTLTLOSLTIGSSSEPPSAVTIKSWDKMOEDLTAKTASGVQLVDIYE 62
Qy 72 EYEDVAIEIDGLQIVKRLAKMEEMFHKSEAVRLVEAEALAKHEFDADL---QY 128
Db 63 KYQDLYTVEPNNAQQLVELIARDIEKLNSRKALVSALAEKQAAMQMRDPAFMSNEV 122
Qy 129 EYFNAVLIERKDKGNFELGKEFT--LAPNDHNNLPVNISLSVOVPTNNKNDPAI 185
Db 123 VYVNAK--DDLPPEKNDSEPGSQRIKPFVIEDANFGR-OISYOHAAVHIPTDIYESSTIY 179
Qy 186 VNGVYVSESLNVFYDNPDRPSLIMQVGSAGKGFROYPGIWEDEE---NGVIAFDCR 242
Db 180 LMEIWNLSALDEVFKKNREEDSLMQVGSATGLAKRYTPASWVUNSKRTPNKIDILYDR 239
Qy 243 NKKWYIQAATSFRDVAIIVDVGSMKGLRLITAKQTVSSILDTGDDFFNITAYNEELH 302
Db 1031 NKKWYIQAATSFRDVAIIVDVGSMKGLRLITAKQTVSSILDTGDDFFNITAYNEELH 302

A:Status: preliminary
```


QY 457 -----IDSTLTDGQVLMNTVAMPVFSKONETRSGILLGVGTDPVVKEL 503
DB 478 SFAVANKMASRRKIRLOKSEARSFMVTYSEYVIT--VNET-----FNGVAAYNIPUTEY 530
QY 504 LKTIPIKYLIGHYAFATINNGYILTHPELRLIYEGRKKRPNSSVDISEVEMEDRDD 563
DB 531 AKSHHPANIGSGSYFFMLDQNGFVMTHPOLRPI-DFPTKYHKONYNMOLLEIEVQONON 589
QY 564 VLRNANVRNKRKTGFSME-----VKKTVDKG-----KRY 591
DB 590 V-RSSQSKQAVSDLVCESGANYAECDVDRKAVRKMIIDCNSDVQOQLVLYATELLDRY 648
QY 592 LVMTNDYYTDDIKGTFPSLGVALSRLG-----HGKYFRGVNTIIEGHLDEHPDVSL 643
DB 649 YQQTNTYAECEINHANFVGLAVAKGDYRVYKKQKKYDF-GKVKMD-----NM 696
QY 644 ADE-WSYCNTHLPEHRHLSQLEAIK---LYLKGEPLL 678
DB 697 GDKRMR-----LHP-HMHWYLFEPFEKPFDMKTYIKVAKPLV 730

RESULT 6
18770
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R:Stulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: 219019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residue type: DNA
A:Residues: 1-1148 <W11>
A:Cross-References: EMBL:249907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone B0491
R:Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: 220004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residue type: DNA
A:Residues: 1-1148 <W12>
A:Cross-References: EMBL:249912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6
A:Experimental source: clone T24F1
C:Genetics:
A:Gene: CESP:T24F1.6
A:Map position: 2
A:introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 9.9%; Score 561; DB 2; Length 1148;
Best Local Similarity 21.3%; Pred. No. 1e-26;
Matches 248; Conservative 213; Mismatches 441; Indels 260; Gaps 49;

QY 17 LLAALALYALGDVNR-SEQQIPLSVVKLWASAGGEIKSIAKYSGS-----Q 64
DB 76 VLVHCIFYYYIGFWLRLSLPLVDIE-----EAPASIAQFSANILRDETOSRFS 127
QY 65 LLOKKKEKDYAEIREDIGLOLVKRLAKNMEMEFKKSAAVRLVEAF-EAHLHHEFD 123
DB 128 LVQEEFEKLKPDIKSKKEDNAEKLVAATEHLDLVTNRDALKKLASAASAAVFEYD 187
QY 124 -----ADQYEVNNAVILNERDKGNFLGKEFIILAPNDHF-NLFPVNISLSDVQY 174
DB 188 DQAYAVPQADKRCQAYAMKKM-NESDM-----HFSNVNVEHNSKSGIHI 229
QY 175 PIRMYKDDAIYNGVY--SESINKYFVNDFRDPQLIMQYFESAGCFQYQYGIKW--E 230
DB 230 TVESYQCDPRVAKDFMTGTKHLKETSNDKNEKAPEMGHQYIGTYSGLTRMYPRRHAKVE 289
QY 231 PBENGVIADCRNRKMYIQATSPKDVVILLVDSGSMKGLRLIACQTVSSILDITGDD 290

DB 290 PPTITIDLPFRRPRPMVNVNNAESVPKDIVFLDLSGSGKGTMLHIKTMVILSTLSPND 349
QY 291 FENIIAYNEELHYVEPLCLNTLVQADRTNKEHREHLDKLPK-----GICMLD 339
DB 350 YFGVGVFNHNFNPLISCANRTFMPATSNKKKFFEEELGMLKEKQDAHFAPPLKFSLDVLR 409
QY 340 IALNEAFNILDPNHHGQSGISCSQAIMLITDGAVDYDTITPAKYNMP-----D 387
DB 410 GNLDNSQSLADYRSEGH-----KLIIFTDG--VD-----EMWHQILDEEFQTRNS 454
QY 388 RKYRIFFYLIGRAAFADNLKMMACANKGFEFTQISTLADVOENMEYLHLSRPKYD-- 445
DB 455 ELIRIFGSMGYGTSLPLQOYMAKCKSHGYSSEIDSLMDYKPSQRTIQNTLSVGRGELK 514
QY 446 ----QEHVVYTAAYIDSTLTDGQVLMNTVAMPVFSKONETRSGILLGVGTDPVVK 501
DB 515 GTNAEKREPSMTQLYME---TQGTGPV--TSLPITLSBQRIWRDQKLAGVAIDISIK 569
QY 502 ELKTIPIKYLIGHYAFATINNGYILTHPELRLIYEGR-KRRKPNSSVDLSE----- 555
DB 570 EFTKHLPTSSQMYGY--IVDNGMLIYHPOLIPKTEVHCVRSSACYDAQVAKQKAGSG 627
QY 556 --VEMEDRDVLRNANVRKKTG-----KESMEYKKTIV--DKGRVLVMT----- 595
DB 628 LRHYHGFSD-----RYRLVGLDITPTLMDLDEDSFRAIRLRRIITTKCYEAIK 682
QY 596 ---NDYYTDDIKGTFPSLGVALSRLGKGKYPFGVNTIIEGHLDEHPDVSLAD----- 645
DB 683 DNSKEYCHSIKDSPTFLVIV-----NNIQKTYVYDSDVQELGTQKVLTFE 731
QY 646 -----EMSYCNTHLPEHRHLSQLEAIKLYLKGEPLLQCKEL---IQEVLFDVVS 695
DB 732 YPRRDVQOMRLDEYAADRFRWSDISE-----KEICADDMRLPRAFTKGISGWTQS 784
QY 696 AP---IPAYVTSIALNKSEMSDKGVEY-AFLGRTGSLRINLFGABQL--TNODF---L 746
DB 785 WPKSDIE-HTTCLLAQYEPENASVPHYVNSFVHRSKLTATAYPCSSHDMKAVKKPDEI 843
QY 747 KAGDKENIFNADHPPLMYRRAEQIPGSFVYSIPFSTGPVKNKSNVYASTSIOLLDERKS 806
DB 844 KLTDNNDF-----VQFSM-----RSESLIYRTIADYDNNR- 874
QY 807 PVAAVGIGOMKLEFQFKFTASRQCASLDGKCSISODDETVCYLIDNNGFIIVSBDY- 865
DB 875 --LAVGTQMKNEFFQDYFNFTRO--NPWKI--CRKO--ECSTIRNGHYATSSAHR 925
QY 866 --TOTGDFGEI-EGAVMNLITFGSPFRITLYDYQAMCRANKESSDGAHGLDPYNAFL 922
DB 926 APLHLAKFDQLESLYKVLVINSTVEY-----QSECKAKR-----VAPWSSAA 971
QY 923 SAYKWMTELVLFLVEFNCSWMHSDM-----TAKAKIKOTLEPCDTE 966
DB 972 PGSSSLIRYVTSIFLAKTSFMRNLLESALTIVDAQPSMTGNCTPQKIK-PRERCFMK 1030
QY 967 YPAFVSERTIKETGTNACEDCSKSFYIQIIPSSNLFMYVYDSCCLCESAPITMAIEI 1026
DB 1031 FFYHRMTLNTKQQLTQMGSTGSRYAKLVPVPHITSLIADRA--CSQYRPKRIFESEP 1088
QY 1027 RVNSLKCERLAKOKIRRPES 1048
DB 1089 RKEE--KCDVYVHSH-ARRRPA 1107

RESULT 7
C86880
hypothetical protein yycC [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. Lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86880
R:Polocin, A.; Wincker, P.; Mager, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

Db 969 NNSSEFVKEVDSLQDKRRTDIASFQANIDITLDSLNVKFN 1009

RESULT 15

JC5574

Inter-alpha-trypsin inhibitor heavy chain 1 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000

C:Accession: JC5574; PC4484

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Shinohara, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors

sin inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688

A:Accession: JC5574

A:Molecule type: mRNA

A:Residues: 1-914 <NNAK>

A:Cross-references: DDBJ:DB9285; NID:91694687; PID:BAAL3938.1; PID:91694688

A:Experimental source: liver

A:Accession: PC4484

A:Molecule type: protein

A:Residues: 387-400:461-475 <NNA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were

that the complexes play important role for pancreatic cancer.

C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

F:247-250,690-890/Disulfide bonds: #status predicted

Query Match 2.7%; Score 152.5; DB 2; Length 914;

Best Local Similarity 21.7%; Pred. No. 0.25;

Matches 95; Conservative 73; Mismatches 174; Indels 95; Gaps 20;

```
OY 47 SAFGEIKSIKAKYSGSLQKKYKEYKDVAIEIDGLQYKKLAKNMEK----- 98
Db 110 NTFIGDIDKAS-----AMQYKRAISGENAG--LVRTSGRMEDQTTIITVGA 156
OY 99 -----FHKKSEAV--RRLVE-----AAEEAHLKHEFDADLOEYFNNAVLINERDKGNFL 146
Db 157 QSKATFQLTVEYELKRRITQYDIKVKPKQLVQHFEIDV--DIPEPGISIKLDAQASF 214
OY 147 --ELGKEFTLAPNDHFNLPYNISLSDYQVPTNMTNKPATVNGVYSESLNKYFVD-NF 203
Db 215 SKELAAQTI--KESFSGKKGHLER---PTVSQOQPCPTCSTSWLNGDFKYTYDVNR 267
OY 204 DRDPSLIQWYGSAGKGFROYGFIKMEPDENGVIADFCCRNKMYTQAATSPKQVYILVDV 263
Db 268 DKLCDL-----VANNYFAHF-----FAPKN-----LTNMSKNLVFVIDI 302
OY 264 SGSNKGRLRTIAKQTVSSILDTLGD--DDFNIIAYNEELHYEPCUNGTLVQADR 320
Db 303 SGSMGQGV--KQTKKALIKILGDVKPGDSFDLVLFGRVQ---SWKGSIVPATQANL 355
OY 321 EHFRHLDKLEAKGIGMIDLNEAFNLSDFNHTGGS---ICQATMLI-----TD 370
Db 356 QAADDFARFSLAGATNLNGSLRGIEL---NKAQGSHPELSSPASILMLTLDGEPT 411
OY 371 GAVDTYDTIFAKYMPDQKVRITFTYLIGREAFADNLKWMACANGFTQISTLADVOEN 430
Db 412 GETDRSQILKAVRNAIRGFLPYNLNGFHDLD-FNLEVMSENGMAGQRIYEDHDATQ 470
OY 431 VMEXLHVLSPKVIDQE 447
Db 471 LGFYNGVAVNPLTDVE 487
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Search completed: August 16, 2002, 22:20:43
Job time: 7128 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 22:19:16 ; Search time 61.26 Seconds
(without alignments)
685.777 Million cell updates/sec

Title: US-09-787-657-5

Perfect score: 5667

Sequence: 1 MAGPSPRRASRGASALLAA.....SLQAQIVLILPLLLMFSR 1085

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1148.5	20.3	1106	C1C2_RABIT	P13806 oryctolagus
2	1122.5	19.8	1091	C1C2_HUMAN	P54289 homo sapien
3	1114.5	19.7	1091	C1C2_RAT	P54290 rattus norv
4	716.5	12.6	734	1 UN36_CAEEL	P34374 caenorhabd
5	167.5	3.0	935	1 ITH2_PIG	002668 sus scrofa
6	166.5	2.9	886	1 ITH3_MOUSE	061704 mus muscu
7	162.5	2.9	886	1 ITH3_MESAU	P97280 mesocricetu
8	156.5	2.8	946	1 ITH2_MESAU	P97279 mesocricetu
9	156.5	2.8	946	1 ITH2_MOUSE	061703 mus muscu
10	154.5	2.7	946	1 ITH2_HUMAN	P19823 homo sapien
11	152.5	2.7	930	1 ITH1_MESAU	P97278 mesocricetu
12	151.5	2.6	930	1 ITH4_HUMAN	Q14624 h inter-alp
13	148.5	2.6	1296	1 ITH3_RAT	063416 rattus norv
14	146.5	2.5	911	1 SC4A_CICLO	008393 plasmodium
15	143.5	2.4	911	1 ITH1_HUMAN	094616 rickettsia
16	137.5	2.4	911	1 ITH1_MOUSE	061702 mus muscu
17	136.5	2.4	907	1 ITH3_HUMAN	006033 homo sapien
18	135.5	2.4	885	1 ITH3_MOUSE	008372 plasmodium
19	134	2.3	3135	1 S230_PLAFO	P35221 homo sapien
20	132.5	2.3	906	1 CTN1_HUMAN	P17699 porcine rot
21	132.5	2.3	1088	1 RRO_ROTPO	029052 sus scrofa
22	130	2.3	902	1 ITH1_PIG	P22678 simian 11 r
23	129	2.3	1088	1 RRO_ROTPO	P22678 sus scrofa
24	127.5	2.2	921	1 ITH4_PIG	P79263 sus scrofa
25	127.5	2.2	1584	1 U104_CAEEL	P23678 caenorhabd
26	127.5	2.2	1636	1 BRD3_YEAST	P25558 saccharomyc
27	127	2.2	1088	1 RRO_ROTPO	P17468 bovine rota
28	127	2.2	1957	1 YDB6_SCHPO	010411 schizosacch
29	127	2.2	2366	1 TOXB_CLODI	P18177 clostridium
30	126.5	2.2	906	1 CTN1_MOUSE	P26331 mus muscu
31	126.5	2.2	1129	1 YB95_YEAST	P38144 saccharomyc
32	125.5	2.2	779	1 CN10_HUMAN	O9Y233 homo sapien
33	124	2.2	1088	1 RRO_ROTPO	P21615 bovine rota

34	124	2.2	4092	1 DYHC_YEAST	P36022 saccharomyc
35	123.5	2.2	944	1 Y166_UREPA	O9PXX7 ureaplasma
36	123	2.2	810	1 CLPC_BACSU	P37571 bacillus su
37	122.5	2.2	1391	1 RPOB_MYCPN	P78013 mycoplasma
38	121.5	2.1	1033	1 SN11_YEAST	Q12038 saccharomyc
39	121.5	2.1	2105	1 POIR_ASQVP	P36309 apple stem
40	121	2.1	917	1 SYI_STRAU	P41972 staphylococ
41	120.5	2.1	5147	1 FAT_DROME	P33450 drosophila
42	119.5	2.1	1451	1 SPTE_YEAST	P23615 saccharomyc
43	119	2.1	1155	1 RPOB_BORBU	Q59191 borrelia bu
44	119	2.1	4568	1 DYHC_CAEEL	Q19020 caenorhabd
45	118.5	2.1	997	1 Y414_MYCPN	P75183 mycoplasma

ALIGNMENTS

RESULT	1	STANDARD	PRT	1106 AA.
AC	C1C2_RABIT			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.			
DE	CACNA2D1 OR CACNA2A OR CCHL2A.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88336904; PubMed=2458626;			
RA	Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H., Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A., Schwartz A., Harpold M.M.;			
RA	"Sequence and expression of mRNAs encoding the alpha 1 and alpha 2 subunits of a DHP-sensitive calcium channel.";			
RT	Science 241:1661-1664(1988).			
RL	[2]			
RN	SEQUENCE OF 961-973.			
RP	MEDLINE=91131638; PubMed=1847144;			
RX	J. Biol. Chem. 266:3287-3293(1991).			
RA	Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M., Campbell K.P.;			
RA	"Structural characterization of the dihydropyridine-sensitive calcium channel alpha 2-subunit and the associated delta peptides.";			
RT	J. Biol. Chem. 265:14738-14741(1990).			
RL	[3]			
RN	SEQUENCE OF 961-975, 992-1000 AND 1033-1050.			
RP	MEDLINE=90368635; PubMed=2168391;			
RX	de Jongh K.S., Warner C., Catterall W.A.;			
RA	"Subunits of purified calcium channels. Alpha 2 and delta are encoded by the same gene.";			
RT	J. Biol. Chem. 265:14738-14741(1990).			
RL	[4]			
RN	FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.			
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	- TISSUE SPECIFICITY: SKELETAL MUSCLE.			
CC	- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.			
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.			
CC	- SIMILARITY: CONTAINS 1 VWF A DOMAIN.			
CC	-----			
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[illegible]

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Db      63 KYODLYVEPNNAQOLVEIARADIEKLLNSRKSALVSLALEAKVOAHQMFEDPASNBY 122
Qy      129 EYFNAVLINERDKGNFLELQKEFI--LAPNDHFNNLPUVNLISLDVQPTMMYKNDPAI 185
Db      123 VYNNK--DLDPEKNDSEFSQOKIRKVFLEADNPGF-QISQOHAHVHTPTIDYEGSIVT 179
Qy      186 VNGVYSESLKVFVDNFDHDPSSLIMQYFGSAGGFQRYQGIKWEDE--NGVIAFDOR 242
Db      180 LNELNWTSLADEVEKKNREEDPSILMVOFGSATGLARYYPASPMWNSRTPKIDLYDVR 239
Qy      243 NRKWIQOATSPKROVVLIVDVGSGMKRLRTIKOVYSSLDITDGDDEPFNIIANDELH 302
Db      240 RRPWYIQOASPKMLILVVDGSGVSLTFLKLRISVSEMLETSLDDVDVNVASNSNAQ 299
Qy      303 YVEPTLNTVLQADRTKNEHREHLQDLPFKGIGMDIAUNEAFNLISDFNHTGGSGIS 362
Db      300 DVS-CFO-HILOVANRRKKVYLKQADVNNTAKGITTDYKKGSFAFBDLNVANSRAN--CN 355
Qy      363 QAIMLITDGAVDYDTJFAKYNMEDRKVRITFLYIGREAAFDNLKMMACANKGFEFTOIS 422
Db      356 KILMFTDGGEGERAQOEIFNNKYN-KDKKVYFRFSSVQGHVNERGPIQUMACENKGYEIEP 414
Qy      423 TLADQVENVMYLVILVSRPKY--DOHDVVMFEAYIDSTLDDGQPVLMFTVAMPVS- 479
Db      415 SIGAIRITQYLDVILSRPWLADKKQOVMNVYLDL--ELG-LVITGLTPVENI 469
Qy      480 ---KONETRSKG-ILGVGVDYVVKELLTIPRYKLGIGHYAFATLNGGYTLTHPELRL 535
Db      470 TGOFPENKLNKLQILIGVMGYDVSLEBIRKLTFRFLPCRGYTFALDPNGYVLLHPNQ- 528
Qy      536 LYEEGKKRRKPNYSSVDLSEVEMEDRDV-LRNAMVNRKTGK--FSMEVK---KTVDKG 588
Db      529 --PKPKSQEP-VTLDFLAELENDIKVEIRKMKIDGEGEXTFTLVKSDERYIDKG 584
Qy      588 KRVLMTMDYTYTIDIKTPPSLGAALSRGKGF-----RGVNTIEBL- 633
Db      585 NMT-----YMTVNGTIDYSLALVLEPT-SPFYIAKLEETITQARSKKGMKSEFLK 637
Qy      634 -HDLHPDVLADMSVCNMDLPHREHRLSQLFAIKLYLKGREP-LLQCDKELIOEVFLD 691
Db      638 PDNFEESSYTLIARDYCN-DLKSIDNNTFELNPFNEFIDRKTPNNPSCNADLIRKVLDD 696
Qy      692 A-VVSAPLEAYWTLALNKSENSDKGEVAFICRTGLSRINLFWGAEOILTNODELKAGD 750
Db      697 AGFTNELVQNWYS-----KOKNIKGYKARFVVTGDIRPVYP-----KEAGE 738
Qy      751 KENIFNADHFPLKRRRAEOIPGSEFVYSIFP--STGPYKSNVYVASTSIOULDERKSPV 808
Db      739 NMQENPETYEDSFKRSIDN--DNVETAFYFKSPSGPYAGESGINVSKAVEYIOTGKLK 796
Qy      809 VAAVGIOKLEFPQKRFMTASROOASLDKCSISCDDEYVNCYLIDNNNGFIVS--EDYT 866
Db      797 PAVYGKIKDVMSTLENFTKTSIRPCAGPAPCDCKRNSDVNDYIILDDGFFLMAHHDYT 856
Qy      867 -QTGDGFEIGEGAVMNKLLTNGSEFKRTILYDQAMCRANKESSDGAHGLDDPY----- 918
Db      857 NQIGRFPGEIDPSLMRHLVNI SYAFAFKSYDQYCEBPAGAPQGA-GHRSAYVPSVADI 915
Qy      919 ---NAFLSAVYVMITELVYLVE--NLCSMHSDMTAKAOKLQOTLEPCDTEYPAFV 971
Db      916 LQIGMMWAAAMWSLQOFLSLTFPRLLAEVEMEDDFTASLSK-----QSCITQOTQYF 970
Qy      972 SERTIKETGTALACEDSKSVFIOQIPSNLPMVWYDS--SCICESVAPITMAPIEIRYN 1029
Db      971 FDNDSKPSGVLDCGNSCRIFHGKELMNTNLITIEWSKTCPCDTRLLLOAEQJSDQPN 1030
Qy      1030 ESLKESIRKAOKIRRPESCHGFEPENARECGASPLAQOT--VLLLPPLMLMS 1084
Db      1031 ---PCDMWKQGRYRKGPDYVCDDNNVLEDYIDGCGVGLNPSLWYIIGIQFILLMYS 1084

```

ID	CITC.RAT	STANDARD:	PRT:	1091 AA.
AC	PF4530:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.			
GN	CACNA2D1 OR CACNA2A OR CCH2A.			
OC	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92228762; PubMed=1314383;			
RA	Kim H.L., Kim H., Lee P., King R.G., Chin H.;			
RT	"Rat brain expresses an alternatively spliced form of the			
RT	dihydropyridine-sensitive L-type calcium channel alpha 2 subunit."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).			
CC	-1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN			
CC	EXCITATION-CONTRACTION COUPLING.			
CC	-1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:			
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS			
CC	HEXADIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE			
CC	SPLICING.			
CC	-1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM			
CC	A PRECURSOR FORM (BY SIMILARITY).			
CC	-1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.			
CC	-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: M86621; AAA41088.1; -			
DR	InterPro: IPR004010; Cache.			
DR	InterPro: IPR002035; VWFA.			
DR	Pfam: PF02743; Cache; 1.			
DR	Pfam: PF00092; vwa; 1.			
DR	SMART: SM00327; VMA; 1.			
DR	PROSITE: PS50234; VWFA; 1.			
KM	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KM	Calcium channel; Glycoprotein; Phosphorylation; Signal;			
KM	Alternative splicing.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	944	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
FT	CHAIN	945	1091	(BY SIMILARITY).
FT	CHAIN	945	1091	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT	TRANSMEM	445	468	POTENTIAL.
FT	TRANSMEM	506	930	POTENTIAL.
FT	TRANSMEM	1067	1086	POTENTIAL.
FT	DOMAIN	252	429	VWFA.
FT	CARBOHYD	92	92	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	323	323	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	347	347	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	584	584	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	593	593	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	663	663	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	769	769	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	812	812	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	876	876	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	883	883	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	973	973	N-LINKED (GLCNAC . . .) (POTENTIAL).

[illegible]

RESULT	ID	UN36_CAEEL	STANDARD;	PRT;	734 AA.
AC	P34374;				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Protein unc-36.				
GN	UNC-36 OR UNC-72 OR C50C3.11.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea				
OC	Rhabditidae; Pelodierinae; Caenorhabditis.				
XC	NCBI_TaxID=6239;				

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2:
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Lalster N.,
RA Larelle P., Lighting J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J.,
RA Wohldman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb.ch.
CC -----
CC EMBL: L14433; AAA27969.1; -.
DR PIR: S44617; S44617.
DR Wormpep: C5OC3.11; CE00117.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache; 1.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; VWFA; 1.
DR PROSITE: PS50234; VWFA; 1.
RW Ionic channel; Ion transport; Voltage-gated channel. Calcium channel;
FW Glycoprotein.

Query Match	12.68;	Score 716.5;	DB 1,	Length 734;
Best Local Similarity	27.9%;	Pred. No. 1.1e-37;		
Matches 212; Conservative	133;	Mismatches 276;		
				Indels 139; Gaps 26

QY	23	LYAAGDVVRSSQOQLP	LSVTVLMSAPGCEGLKSLIAAYSSGGLLOKKYKKEKQVLALEI	82
Db	6	LIVLVATVYVSTSSFNKESIE	CECAVUSSEHKKEFTPSKHETLTK---	QNTKLEVEEOF 62
QY	83	DGLQVKKLAKMMEEMFHKSE	EAARLVEAAEHALKHEPDA-DLQYEFNAVLINERDK	141H
Db	63	DEPRLKTSKSHRIEDY	LKVRSQAPYKAKISLEARSVNRDSYVNDPQSKSFLIREMSAQGN	1222
QY	142	DGNEL-----ELG-----	KEFLARPNDHFNLPVNISLSDOVPPNMTNKDPALYNGV	188H
Db	123	DGTTYESNNHLGKRLKLVNET	SFNLTOANFYTLPTSSSVSAVHIPPLDYRNEDLIRKI	182H
QY	190	YMSSELNVFVNDPNRDSLSL	IMQYFGSKAGFFROYPGK--WEDDENGVALAFQCRNRKW	247H
Db	183	DMSD-IDVAVYTRNREYTKDL	FLQFCSAGYMRKYPAASWMDQDEHLDFDRNTEWY	241H
QY	248	IQAAATSPKDVVILVDSGSGM	KGLRLTTAKQVSSILDTLGDDEFNTIAYNEELHYEPC	307H
Db	242	INSATNSKNVLIMLDMSGMS	IGORYEVAKQYTEALILETLSHNDYFNIMTFSKNFTLLDGC	301H
QY	308	LNGT--LVQADRTKNEHREH	LDLFLAKGIGMDIALNEANILSDPNHTG---QSSICS	366H
Db	302	NGTNGLLQATMRNKKALRR	KMDYQSGKAYEKALPLAASVLLDINNGGDNNGACE	360H
QY	363	QAIMLITDGAVDYDTIEFAK	YNMPPRKVRIPTYLIGREAPADMLKMACANKGFTYOIS	422H
Db	361	NVIMLITGAPRAYKKIFDMY	N-ADKRVRYTFVLGDIDAIDFNEVREMACNNGYVYHVA	419H
QY	423	TLADVOENVMEYLHLSRPKY	IIDDBHYV-----WTEAY-----	456H
Db	420	NMADVDEKIHNYIRKMSR--	VVGRYKYESGOLSWTGYRERLPLPREPIFAEPVPTNQ	477H
QY	457	-----IDSTLTDGQVLM	TPMVPFESQNEFRSGILGIVGTQVPAKEL	503H
Db	478	SFAVNNKMASRRKILQKSE	RSKRFEVTVTSYPIV--VNEI-----FMGVAANVILPLEY	530H
QY	504	LKTIPIKLGIGHGAFATANN	GYILTHEPLILLYEEGKRRKRPYSSVSLDESEVEMEDRD	563H
Db	531	AQSHRANIGSKSYFEMLDQ	NGFVWTHQLRPI-DPFTKYKHQYNNMMDLLELEVGOON	589H
QY	564	VLRANAMVRKTKGKSME---	-----VKTYVDG-----	KRY 591H
Db	590	V-RSSQKQAAVSDLVCE	SGANYABCDVLDLRKAVRKMIIDCNSDOQLVLYATELLDRY	648H
QY	592	LVMTNDYVYTDIKGPTFL	GAVALSRG-----HGKFFRGVNTIEGGLHLEHDPVSL	643H
Db	649	YPQTTTYTAECINAHN	AFVLGLAVAKGDYRYVKKOKKTYDF--GRKMD-----WM	696H
QY	644	ADE-WSYCNTDLHREHRL	SQLEALK---LYLKGKEPLL	678H
Db	697	GDKRMR-----LHP--	HWHVFLFEFFKKNEDMKYIKVKKLPLV	730H
RESULT	5			
ITH2_PIG				
AC	002668;	STANDARD;	PRT;	935 AA.
DT	15-JUL-1998 (Rel. 36, Last sequence update)			

KM Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein. 1 18 POTENTIAL.
 FT SIGNAL 19 30 BY SIMILARITY.
 FT PROPEP 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT CHAIN 31 646 H3.
 FT PROPEP 647 886 BY SIMILARITY.
 FT DOMAIN 279 439 WMFA.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 FT (BY SIMILARITY).
 SQ SEQUENCE 886 AA; 98977 MW; 15955308C7E5030A CRC64;

Query Match 2.9%; Score 166.5; DB 1; Length 886;
 Best Local Similarity 19.6%; Pred. No. 0.0089;
 Matches 160; Conservative 104; Mismatches 255; Indels 297; Gaps 37;

QY 71 KEKDVAVIEIDGLQYKLAEMEM-----FKKSAVRLVAAEAH 117
 DB 110 KQEKAVSOGKTAG--LVYASGRLEKFTVSVVAAGSKVTFELLYELLKRNKGYEM 167
 QY 118 LK-----HEFDALQYEFNAVILINERDGNFLE--LGKEPIAPNDHFNLV 165
 DB 168 LKQVQKQVLRHFIDAH-----FEQGISMLDAASFITDGLSALTKFSQKGVSF 223
 QY 166 NLSLSVQ-VPT--NMVKNDAIVNGVWSESLNKFVDFNDRPSLIMQYFGSAKGF 221
 DB 224 KPSLDQQRSPCTDSTDLNDFIYDVN-RESPGVQIVN-----GYF 266
 QY 222 ROVPGIKMPEDENGVIAFCORNRKWTQATSPKDVILVDSGSKGLTLIAKQVSS 281
 DB 267 VHF-----FAQGLPVV-----PKNIVFVDSGSGMKRIQOTREALK 306
 QY 282 ILDTLGGDDFFNIATNEELHYEPCLTGTVADRTNKEFHREHLKL----- 330
 DB 307 ILDDVAKEDYLNILFSTVD---TTWKDHLVQATPANLKEATFVANINDQSTNTINDG 362
 QY 331 FAKGISMLDIALNEAFNIIISDFNHGOGSICSAIMLTDGAVDYTFITFAKNWPDKV 390
 DB 363 LKKGIMLNKARDD-----HTVPERSTIIML-TGDANTGHSREPKIOENRNA 412
 QY 391 ---RIFTYILIGRAAFADNLK-----MACANGFEFTQISTADVQNVWEYLIVSRP 442
 DB 413 IGGKFFLYING---FGNNLNTNPLETTLAENGLARITIEDSDANIQLQGFYEVAANP- 467
 QY 443 VIDQEHVVTVEAYIDSTILDQGPVLTVMAMPVFSKQNETRSKGIILGVGTGVDPVKE 502
 DB 468 -----LNTNVEYEYENA 480
 QY 503 LKTIKPKYKLGIVAFAITNNGYILTHPELRLLYEGRKRRPNY;SVDLSEVEMEDRD 562
 DB 481 ILD-----LTRNSY-----PHF--YDGSSEI----- 498
 QY 563 DVLARNAMVRKKGFSMEYKKTVDKGRVLYMTNDYYTDIKGTPFSLGVALSHGSKYF 622
 DB 499 -VYAGRLVDRNMDFKADYK-----GNGAL- 522
 QY 623 FRGNVITIEGLDLEHDPVSLADE-----WSYCTDLPHPEIRHLSOLEAFLYLT 671
 DB 523 --NDLFTFEV-DMEEMDALKEQGIIFGDIYERLWAYLT-----IEQLLEKRNA 570
 QY 672 KGEKPLQCDCKELIOEVLVDPAVVASPIEAWTSLANKSEN-----SDKGVFAVFLGT 724
 DB 571 KGE-----KENITAEALDLSLKYHFVPLTSMVYTKKPEDNDQETIAIAGGEAPAE 624
 QY 725 RUGLSRLNLFVGAEOQLNDELKA-GDKENIFNADHPLMYRAAEIIPG--SFVYSIP 780
 DB 625 TT-----MSFLTTQSSQSFYYVVDG-----PHFIT-----DIPKNDISICPNID 665
 QY 781 FSTGPVNR--SNVVTAST-SIQLLDERKSPVNAV 813

DB 666 EKPTVLRLIDPVYTGITVQIIGDKRNSASRTG 701

RESULT 7
 ITH3_MESAU
 ID ITH3_MESAU STANDARD; PRT; 886 AA.
 AC P97280;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
 DE chain H3) (C33).
 GN ITH3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=97420688; PubMed=9276673;
 RX Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
 RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
 RT implications for the evolution of the inter-alpha-trypsin inhibitor
 RT heavy chain family.";
 RL J. Biochem. 122:71-82(1997).
 RN [2]
 RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
 RC TISSUE=plasma;
 RX MEDLINE=97018241; PubMed=8864857;
 RA Yamamoto T., Yamamoto K., Sinohara H.;
 RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
 RT hamster urine and plasma.";
 RL J. Biochem. 120:145-152(1996).
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1- PPM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; D89287; BAI3940.1; -;
 DR InterPro: IPR002035; WMFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; vwa; 1.
 DR PROSITE: PS50234; WMFA; 1.
 KM Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein. 1 18
 FT SIGNAL 19 30 POTENTIAL.
 FT PROPEP 31 646 BY SIMILARITY.
 FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT H3.
 FT PROPEP 647 886 BY SIMILARITY.

Db 424 PTYGLKSLKIQKNVKQIOD-NISLFSIGIFVDY-DFLKRLSNRGIAGRIYGNRD 481
 QY 427 VQENMEYLHVLSRPKYIDQEHVDVWTEAYIDSTLTD 463
 Db 482 TSSQKKFEYNOVSTPLLRNVQFN-----YPOASVTD 512

RESULT 9
 ID ITH2_MOUSE STANDARD; PRT; 946 AA.
 AC Q61703;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2).
 GN ITH2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6N; TISSUE=Liver;
 RX MEDLINE=95194326; PubMed=7534067;
 RA Chan P., Ristler J.-L., Raquenez G., Sallier J.-P.;
 RT "The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain."
 RL Biochem. J. 306:505-512(1995).
 CC -1 FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
 CC -1 SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 CC -1 PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE ITI FAMILY.
 CC -1 SIMILARITY: CONTAINS 1 VMFA DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X70392; CAA49842.1; -
 DR MGD: MGI:96619; Itln2.
 DR InterPro: IPR002035; VMFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; VWA; 1.
 DR PROSITE: PS50234; VMFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 18
 FT PROPER 19 54
 FT CHAIN 55 702
 FT PROPER 703 946
 FT DOMAIN 308 468
 FT CARBOHD 118 118
 FT CARBOHD 263 263
 FT CARBOHD 445 445

BY SIMILARITY.
 VMFA.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 FT SEQUENCE 946 AA; 105927 MW; 40DB6716433ED9DC CRC64;
 SQ

Query Match
 Best Local Similarity 24.5%; Pred. No. 0.042;
 Matches 53; Conservative 56; Mismatches 90; Indels 17; Gaps 6;

QY 254 PKDVTILVDVSGMKGLRLTIKQVSSILDTLGDDFFNIAYNEELAYEPCLANGTLV 313
 DB 308 PKNILEYIDVSGSMGKMGKQVEAMKTIIDDLRTDQFSVDNF--HNVRTRN-DLV 363
 QY 314 QADRTKEHREHLDLFAKIGMDIALNEARNIISDFNHTGQSICS-QALMLITDGA 372
 DB 364 SATKTIADAKRYIEKTIQPSGGTINELRALFILLNEASNMGLNDPDSVSLIILVSDG 423
 QY 373 VDTYDTIFAKYNMPDRK-----VRIFFYLGRFAFADNLKMAKNGEFTQISTLADV 427
 DB 424 PTYGLKSLKIQKNVKQIODNISLFSIGIFVDY-DFLKRLSNRGIAGRIYGNQDT 482
 QY 428 QENMEYLHVLSRPKYIDQEHVDVWTEAYIDSTLTD 463
 DB 483 TSSQKKFEYNOVSTPLLRNVQFN-----YPOASVTD 512

RESULT 10
 ID ITH2_HUMAN STANDARD; PRT; 946 AA.
 AC P19823; Q15484; Q14659;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (inter-alpha-trypsin inhibitor complex component II)
 DE (Serum-derived hyaluronan-associated protein) (SHAP).
 GN ITH2 OR IGHEP2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88152237; PubMed=2450046;
 RA Gebhard W., Schreitmüller T., Hochstrasser K., Wächter E.;
 RT "Complementary DNA and derived amino acid sequence of the precursor of one of the three protein components of the inter-alpha-trypsin inhibitor complex."
 RT FEBS Lett. 229:63-67(1988).
 RN [2]
 RP SEQUENCE OF 384-865 FROM N.A.
 RX MEDLINE=88068576; PubMed=2446322;
 RA Sallier J.-P., Diarra-Mehrput M., Sesboue R., Bourguignon J., Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.-P.;
 RT "Isolation and characterization of cDNAs encoding the heavy chain of human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous evidence for multipolypeptide chain structure of I alpha TI."
 RT Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
 RN [3]
 RP SEQUENCE OF 384-766 FROM N.A.
 RX MEDLINE=89076497; PubMed=2462430;
 RA Sallier J.-P., Diarra-Mehrput M., Sesboue R., Bourguignon J., Martin J.-P.;
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain."
 RT Biol. Chem. Hoppe-Seyler 369:15-18(1988).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88024442; PubMed=3663330;
 RA Schreitmüller T., Hochstrasser K., Resinger P.W.M., Wächter E., Gebhard W.;

RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three
RL different proteins." ;
RN Biol. Chem. Hoppe-Seyler 368:963-970(1987).
RP [5]
RX SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
RN MEDLINE=99380192; Pubmed=2476436.
RX Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RN "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
RT Polypeptide chain stoichiometry and assembly by glycan." ;
RL Biol. Chem. 264:15975-15981(1989).
RN [6]
RP SEQUENCE OF 55-64.
RX TISSUE-Plasma;
RN MEDLINE=93039735; Pubmed=1384548;
RX Melki N., Baldyuc M., Mees P., Capon C., Mizon C., Han K.K.,
RN Tartar A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their
RT isolation, their identification by electrophoresis and partial
RT sequencing. Differential reactivity with concanavalin A." ;
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
RN [7]
RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
RN CARBOHYDRATE-LINKAGE SITES T-691.
RX MEDLINE=93232026; Pubmed=7682553;
RN Enghild J.J., Salvesen G., Thøgersen I.B., Valnikova Z.,
RX Pizzo S.V., Helga S.A.;
RN "Presence of the protein-glycosaminoglycan-protein covalent cross-link
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
RT 2/Dikunin." ;
RL J. Biol. Chem. 268:8711-8716(1993).
RN [8]
RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.
RN TISSUE-Serum;
RX MEDLINE=94075371; Pubmed=7504674;
RN Huang L., Yoneda M., Kimeta K.;
RX "A serum-derived hyaluronan-associated protein (SHAP) is the heavy
RT chain of the inter-alpha-trypsin inhibitor." ;
RL J. Biol. Chem. 268:26725-26730(1993).
RN [9]
RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
RN TISSUE-Plasma;
RX MEDLINE=94229087; Pubmed=7513643;
RN Morelle W., Capon C., Baldyuc M., Sautiere P., Kouach M.,
RX Michalski C., Fournet B., Mizon J.;
RN "Chondroitin sulphate covalently cross-links the three polypeptide
RT chains of inter-alpha-trypsin inhibitor." ;
RL Eur. J. Biochem. 221:881-886(1994).
RN [10]
RP CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
RX MEDLINE=9843966; Pubmed=9677377;
RN Flahaut C., Capon C., Baldyuc M., Riart G., Sautiere P., Mizon J.;
RX "Glycosylation pattern of human inter-alpha-inhibitor heavy chains." ;
RL Biochem. J. 333:749-756(1998).
RN [11]
RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=98087700; Pubmed=945062;
RN Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,
RA Enghild J.J.;
RN "Posttranslational modifications of human inter-alpha-inhibitor:
RT identification of glycans and disulfide bridges in heavy chains 1 and
RT 2." ;
RL Biochemistry 37:408-416(1998).
RN [12]
RP FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SPERM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
CC BIKUNIN, INTER-ALPHA-INHIBITOR (1-ALPHA-1) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC

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CC -!- PTH: HEAVY CHAINS ARE INTERLINKED WITH BIKININ VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
CC -!- MASS SPECTROMETRY: MW=76508; METHOD=WALDI; RANGE=55-702.  
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -!- SIMILARITY: CONTRAINS 1 VWFA DOMAIN.  
-----  
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CC or send an email to license@isb-sib.ch).  
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DR EMBL: X07173; CAA30160.1; ALT_SEQ.  
DR EMBL: M18193; AAA60558.1;  
DR EMBL: M33033; AAA59195.1;  
DR PIR: S00346; IYHU2.  
DR PIR: B34245; B34245.  
DR GlycosylatedB; P19823;. .  
DR MIM: 146640; .  
DR InterPro: IPRO02035; VWFA.  
DR Pfam: PF00092; vwa; 1.  
DR SMART: SM00327; VWFA; 1.  
DR PROSITE: PS50234; VWFA; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 54  
FT CHAIN 55 702 INTER-ALPHA-TRIPSPIN INHIBITOR HEAVY CHAIN  
          H2.  
FT PROPEP 703 946  
FT DOMAIN 308 468 VWFA.  
FT DISULFID 261 264  
FT DISULFID 650 651  
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (COMPLEX).  
FT CARBOHYD 666 666 /FTID-CAR_000140.  
FT CARBOHYD 671 671 O-LINKED (GALNAC. . .) (PARTIAL).  
FT CARBOHYD 673 673 /FTID-CAR_000214.  
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 675 675 O-LINKED (GALNAC. . .).  
FT CARBOHYD 691 691 /FTID-CAR_000215.  
FT MOD_RES 282 282 O-LINKED (GALNAC. . .).  
FT BINDING 702 702 /FTID-CAR_000216.  
FT CONFLICT 374 374 O-LINKED (GALNAC. . .).  
FT CONFLICT 674 674 /FTID-CAR_000217.  
FT CONFLICT 705 705 CARBOXYLYATION.  
FT CONFLICT 729 729 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
FT CONFLICT 731 731 K -> L (IN REF. 5).  
FT SEQUENCE 946 AA; 106436 MW; 147BCF3E8F3BA776 CRC64;  
  
Query Match 2.7%; Score 154.5; DB 1; Length 946;  
Best Local Similarity 23.3%; Pred. No. 0.056; Mismatches 89; Indels 23; Gaps 7;  
Matches 51; Conservative 56;
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QY 425 ADVQENMEXLHVLSPKVIDOEHDVWTEAYIDSTLTD 463
DB 480 QDTSSQKFKFYNOVSTPLLRNVOFN-----YPHISVTD 512

RESULT 11
ID ITH4_MESAU STANDARD: PRT: 914 AA.
AC P97278:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITI heavy
chain H1) (HCl).
GN ITH1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_Taxid=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=9276673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT implications for the evolution of the inter-alpha-trypsin inhibitor
RT heavy chain family."
RT J. Biochem. 122:71-82(1997).
RN [2]
RP SEQUENCE OF 387-401 AND 461-475, AND SUBUNITS.
RC TISSUE=Plasma;
RX MEDLINE=97018241; PubMed=8864857;
RA Yamamoto T., Yamamoto K., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma."
RT J. Biochem. 120:145-152(1996).
RN [3]
RP FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN (BY
CC SIMILARITY).
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITH1 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL, D89285; BAA13938.1; .
CC InterPro: IPR002035; VMFA.
CC Pfam: PF00092; vwa: 1.
CC SMART: SM00327; vwa: 1.
CC PROSITE: PS50334; VMFA: 1.
CC Serine protease inhibitor; Repeat; Signal; Multigene family;
CC Glycoprotein.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 675 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

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FT PROPER 676 914 H1.
FT DOMAIN 293 453 POTENTIAL.
FT CARBOHYD 288 288 VMFA.
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT SEQUENCE 914 AA; 101785 MW; B63JFE956FE89E3 CRC64;

Query Match 2.7%; Score 152.5; DB 1; Length 914;
Best Local Similarity 21.7%; Pred. No. 0.071;
Matches 95; Conservative 73; Mismatches 174; Indels 95; Gaps 20;

QY 47 SAREGEIKSIANKYSGSQLQKKYKEXEKDVAIEIDGLVKKLAKMEEM----- 98
DB 110 NTFIGDIKDKAS-----AMKQYRKAIISGENAG---LVRTSGRMDEFTIHIVGA 156
QY 99 -----FKKSEAV--RRIVE-----AAEBAHKHEFPADLOEYFNVLINERKDGNFL 146
DB 157 QSKATFQLTYEEVLKRLTGYDIYIKVPRQOLVOHFEIDV--DIEPQGISKLDAQSFL 214
QY 147 --ELGKEFIAPNDHFNNLPVNIISLSDVOYPTNNYKNOPAVNGVYSESINKVFVD--NF 203
DB 215 SKELAAQTI---KESEGGKGVLF---PTVSQOQOQPCPTCTSLNDEKVTYDYNR 267
QY 204 DRDPSLIWOYFGSAGGFROYPGIKWEPDENGVAIFDCRRKRWYIOAATSPKDVILLVY 263
DB 268 DKLCDDL-----VANNYFAHF-----FAPKN-----LTNMSKNLVFVIDI 302
QY 264 SGSKGKLRLTAAQTVSIIIDTLD---DFFNIATANEELHYEPLCLNGLVQADPTNK 320
DB 303 SSGSREGKV--KQTKALLKILGDVKGPSFDVLGSRVQ---SMKSLVPATQANL 355
QY 321 EHFREHDKLFPAKIGIMDLALNEAFNLSDFNHTGGSS---ICSQAIML-----TD 370
DB 356 QAAQDFYRRSLAGATMLNGSLGIEIL-----KKAQSHPELSSPASIIMLTGDEPTE 411
QY 371 GAVDTYDTIFAKYMPDPKRYRIFTYLLIGREAFADNLKMAACANKGFTQISTLADVOEN 430
DB 412 GEFTRSQILKNVRNAIGRPFLYMLGFGHLDL--NFLFVSMENSGMARTEYEDHDAQ 470
QY 431 VMEYLHVLSPKVIDOE 447
DB 471 LOGEFYNOVANPLDLDVE 487

RESULT 12
ID ITH4_HUMAN STANDARD: PRT: 930 AA.
AC Q14624; Q15135; Q9U054;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy
chain H4) (inter-alpha-trypsin inhibitor family heavy chain-related
protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (PK-
120) (GP120) [Contains: GP57].
GN ITH4 OR IHRP OR ITIH1 OR PK120.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=95293915; PubMed=7775381;
RA Saguchi K.-I., Tobe T., Hashimoto K., Sano Y., Nakano Y., Miura N.-H.,
RA Tomita M.;
RT "Cloning and characterization of cDNA for inter-alpha-trypsin
RT inhibitor family heavy chain-related protein (IHRP), a novel human
RT plasma glycoprotein."

```

RL J. Blochem. 117:14-18(1995).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-LIVER:
RX MEDLINE-95104473; PubMed-7605892;
RA Nishimura H., Kakizaki I., Muta T., Sasaki N., Pu P.X., Yamashita T.,
Nagasawa S.;
RT "cDNA and deduced amino acid sequence of human PK-120, a plasma
RT kallikrein-sensitive glycoprotein.";
RL FEBS Lett. 357:207-211(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96389935; PubMed-8797089;
RA Saguchi K., Tobe T., Hashimoto K., Nagasaki Y., Oda E., Nakano Y.,
Mura N.H., Tomita M.;
RT "Isolation and characterization of the human inter-alpha-trypsin
RT inhibitor family heavy chain-related protein (IHRP) gene (ITIH1).";
RL J. Biochem. 119:698-905(1996).
RN [4]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE-Plasma;
RX MEDLINE-95332266; PubMed-7541790;
RA Chot-Mura N.-H., Sano Y., Oda E., Nakano Y., Tobe T., Yanagishita T.,
Tanuyama M., Katagiri T., Tomita M.;
RT "Purification and characterization of a novel glycoprotein which has
RT significant homology to heavy chains of inter-alpha-trypsin inhibitor
RL family from human plasma.";
RL J. Biochem. 117:400-407(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY IN THE SERA OF PATIENTS
CC AFTER DIFFERENT SURGICAL TRAUMA.
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 100- AND 35-KDA
CC FRAGMENTS, AND THE RESULTING 100-KDA FRAGMENT IS FURTHER CONVERTED
CC TO A 70-KDA FRAGMENT.
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D38595; BA07602.1; -;
DR EMBL: D38535; BA07536.1; -;
DR EMBL: U43163; AAD05198.1; -;
DR EMBL: U42015; AAD05198.1; JOINED.
DR EMBL: U42016; AAD05198.1; JOINED.
DR EMBL: U43155; AAD05198.1; JOINED.
DR EMBL: U43156; AAD05198.1; JOINED.
DR EMBL: U43157; AAD05198.1; JOINED.
DR EMBL: U43158; AAD05198.1; JOINED.
DR EMBL: U43159; AAD05198.1; JOINED.
DR EMBL: U43160; AAD05198.1; JOINED.
DR EMBL: U43161; AAD05198.1; JOINED.
DR EMBL: U43162; AAD05198.1; JOINED.
DR MIM: 600564; -;
DR InterPro: IPR002035; VWFA.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; vwa; 1.
DR PROSITE: PS50234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 661
FT PROPE 662 688
FT CHAIN 689 930
FT HEAVY CHAIN H4.
FT HEAVY CHAIN H4.
FT POTENTIALLY ACTIVE PEPTIDE.
FT 35 KDA INTER-ALPHA-TRYPsin INHIBITOR
FT HEAVY CHAIN H4.

FT DOMAIN 272 432 VWFA.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 696 696 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 701 701 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 702 702 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 747 925 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 85 85 PROBABLE.
FT CONFLICT 85 85 N -> I (IN REF. 2).
FT CONFLICT 114 114 N -> K (IN REF. 3).
FT CONFLICT 207 207 S -> N (IN REF. 1).
FT CONFLICT 221 221 N -> F (IN REF. 4).
FT CONFLICT 307 307 Q -> E (IN REF. 4).
FT CONFLICT 322 322 R -> V (IN REF. 4).
FT CONFLICT 322 322 W -> Y (IN REF. 4).
FT CONFLICT 816 817 ET -> Q (IN REF. 4).
SQ SEQUENCE 930 AA; 103358 MW; 0E1929065F4EB6A0 CRC64;

Query Match 2.7%; Score 151.5; DB 1; Length 930;
Best Local Similarity 19.7%; Pred. No. 0.085;
Matches 191; Conservative 125; Mismatches 365; Indels 287; Gaps 45;

OY 67 OKKRYEKEDVAIEEDIGQLVKKLAKNMEHKKSEAVRRLVEAEBAHLKHEPDADL 126
DB EKAEQAQYSAAVAKKSGVAKATGRNMEQF-----QYSSVAAPNAKTIFF-----L 144

OY 127 QIEYFAVVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 145 VYE---ELKRR-----LGVYELLKVRQQLVKHLOMDIHFEPO----- 182
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 184 AIYNGVYSESLUKVVDNDRPDSLIMQYFGSAKGFEPYQIKMEP-----DE 233
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 183 -----GISFLET--ESTPTQQLDALTTWQ--KTKAKHFKPPLSQQSQPEQEVYLDG 235
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 234 NGVIAPDCR-----NRKWTQ-----AATSPKDVILVDVSGSKGLRLTIARQ 277
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 236 NIIRYDVORATSGSIQIENGFYVHFAPREGLTTPKNNVVFIEKSGMSGRKIQTRE 295
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 278 TVSSILDTGDDDFEITIAVNEELHAYVEPCLNGTLVQADRTKKEHREHLDKIFAKIGM 337
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 296 ALIKILDLSPROFNLIVSTEAQWRP---SLVPASAEVNNKARSPAGIOLAGGTN 351
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 338 LDIALNEAFNLSDFN---HTGSGSICSOAILMTITGAVDTYT-----IFAK 382
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 352 INDAMLMAYQLDSSNOEERLPBGV--SLIILITGDDPTVGETNINRSTONNREAVSGR 409
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 383 YNMPDKRVRIETYLIGREAFAADNLKMKACANKGFTPTQISTLADVOENMEYLHLVSRP- 441
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 410 YS-----LFCIGFGFDVSYA-FLEKLLDNGGLARRIHEDSDALQODFYQEVANPL 461
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 442 -----KYIDEDHVVW--TEAYIDSTLTDOQGVPLMTVAMPFESKONER 485
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 462 LRAVTFEYPSNAVEEYTONNFRLEFGSEMVVAGKL-QDRGPDVLTATVSGKLPTQNTIF 520
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 486 SKGILLGVGTDPVVKELTKTIPKY-----KLGH----- 515
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 521 Q-----TESSVADEAEFQSPKTYFHNFMERLNAVYLITQQLLEQTVASADQOALRN 573
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 516 -----GYAFATNNGVYLTHPELRLLYEEGKKRRKPPYSSVDLSEVEMEDRDVLRNA 568
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 574 QALNLSTLAVSFVTPPLTSNVVTKPDDQ---EQSQVAEKP-----MEGESRN--RNV 618
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 569 MVRNRTKFSMEKVTYDVKGRVLVNTNDYITDITKGTFSGLVALSRHGKFFRGVNT 628
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 619 HSGSTFFKXYLOGAK-----IPKPASSFSPRGWNRQAGAGSRNN-----FRPGVL 665
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 629 IEEGLHDEHPVSLADEWSCNTDLHPHRLHLSQEA-IKLYLKGKPELLCCKDEL-TO 686
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 666 SSRQLGLGPRPV--PDHNAV-----HP-FRLALILPASAPRATSPDPRAVRYNMKKE 717
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

OY 687 EVLFDVAVSAPLEAVYWTSLALNKSNSDKGVEAVFLGTRTGLSRINLFPVGAQO---LTNQ 743
DB IYEFNAVLINERKDKGNLELG-KEPIL--APNDHFNLPVNISLSDOVPTNNYKNKP 183

DB 718 ETTMTOTPAPIQAPSALPL-----PGOSVERLCVDPRHROGPVLLSDPEQGEVETQ 772
QY 744 -DELKAGOK--ENINADHPL-WYRAAEQIPGSEFVSIPESTGPVNSVNTASTSIQ 799
DB 773 YEREKAGSMIEVTEKFN---PLVWVASPEHV-----VTRNRSS 810
QY 800 LLDKSPVAVAVGIOMLFEFGKFWTASRCASLDKCSISCODEIYVNCILIDNNGFI 859
DB 811 AVKMETLEFSVPMGLKMTM-----DKTGIL 835
QY 860 LVSE-DYTOTGDFGEIEGAVNKKL-----TMGSFKRTITLDYOAMCRANKE 906
DB 836 LLSDDPKYITIGLTFWDGCEGLRLLRDRSSHVGLGFIQYDVMGSPA-----A 889
QY 907 SSDGAHL 914
DB 890 SDDGRRTL 897
RESULT 13
ID ITH3_RAT STANDARD: PRT; 887 AA.
AC Q63416;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
GN chain H3).
OS ITIH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA Blom A., Fries E.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X83231; CA58233.1; .
CC DR InterPro: IPR002035; VWFA.
CC DR Pfam: PF00092; vwa; 1.
CC DR SMART: SMO0327; VWA; 1.
CC DR PROSITE: PS50234; VWFA; 1.
KM Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.

FT CHAIN 34 647 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
FT PROPEP 648 887 H3. SIMILARITY.
FT DOMAIN 282 442 VWFA.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT SEQUENCE 887 AA; 99097 MW; 3B9F0FF96D514096 CRC64;
SQ
Query Match 2.6%; Score 148.5; DB 1; Length 887;
Best Local Similarity 17.4%; Pred No. 0.12;
Matches 142; Conservative 127; Mismatches 244; Indels 303; Gaps 37;
QY 60 YSSGOLLQKK--KYEKEDVAIEIDLOLVKLNKME-----MFKKSE 104
DB 101 YPGS-VKEKEVAQKQYKAVSQKTAG--LVKASGRKLEKFTVSVMVAAGSKVIFELTYE 157
QY 105 AVRRLVEAAEAAHLK-----HEFDADLOEYRNAVLINERDKGNFL--LGER 152
DB 158 ELKRRKRGKYEMLKVQPKQVNHFEIDAH---FEQGISMLDADASEITNDLGSAL 213
QY 153 ILAPNDHFNNLPVNISLSVQ--VPT---NMYNKDPALVNGVYSESLNKVFVDFNDRPS 208
DB 214 TRFSQKKGHVSKRPSLDQORSCPTCTDILNDFTIYIVN--RESPGNQIYN----- 266
QY 209 LIWQYFSAGKGFPRQYPGIKWEPDENGVIADFGRNRKMYIOAATSPKDVVILVDSGSMK 268
DB 267 -----GYFVHF---FAQGLPVV-----PRNIAFVIDVSGSMS 296
QY 269 GLRLITAKQTVSSILDTLGDDEFFNIIAYNEELHYEPCNLGVQADRNRKHFREHL 328
DB 297 GRIQOQREALKILDDMKEDYDLNFTSTGV---TWKDLVATPANELAARFVK 352
QY 329 KL-----FAKGIGLIDALNDAFNIHIDFNHTGSGISCSQAIMITDGAVDYD 377
DB 353 NIDRSMTNINDGLNGIEMLNKARED--HLVERS-----TSLVMLTGDANTGE 402
QY 378 TIFAKYNWPDRAV--RIETYLIGREAAFAADNLK---MACANGGFQIOTLADVOE 429
DB 403 SREKIQENVRNMIIRKFKPLVNG---FGNNLVNPLESLALENHGFARIYEDSDASL 458
QY 430 NWMEYLHLSRPKVIDDEHDVYVTEAVIDSTLTDGQPVLMITVAVPFSKQNETSKGI 489
DB 459 QLOGFYEEVAVNP-----LLTNVEL----- 477
QY 490 LIGVGADVPVKELKTIPKKGIGYAFATNNGIILHPRLLYEGRKKRRPNYS 549
DB 478 -----EYDENALD-----LTRNSI-----PHF- 495
QY 550 SYDLSEVEMEDRDVLRNMAVNRKTKFSMEVKYVDKGRVLVMTNDYYTIDIKTPFS 609
DB 496 -YDGESEI-----VVAGRVLDNRVDFNKADV----- 520
QY 610 LGVALSRGRHKYFRGNVNTIEEGHDLHPDVLAD-----WSYCNMIDLHPH 658
DB 521 -----GREAL--NDLFTTEEV--DMKEMDALKEQGYIFGDI IERLWAYLR----- 562
QY 659 RHLSQLEAIKLYGKREPLLOCDELIQEVLPFAVVSAPIEAWTSLALKSENSDKGVE 718
DB 563 --IEQLLEKRNKRGD-----KENTATALELSLKYHVTPLTSVNVYKPPEDNEDQTA 614
QY 719 VAFLGTRTGISRLNLFVGAEQLTNODFLKAGDKENIFNADHPLMYRRAAEQIPGS--FY 776
DB 615 IADKPEEALASASTAYLTSQ-----SSHSPPYY-----VDGDPHF 651
QY 777 YSIPFSTGPVNSVNTASTSIQLDERKSPVAAV 812
DB 652 IQVP-----GKNDTICFN-----IDKKPTVLSLI 676
RESULT 14

BXG_CLOBO STANDARD: PRT: 1296 AA.

AC 060393: DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

De Botulinum neurotoxin type G precursor (EC 3.4.24.69) (Bont/G)

De Bontolysin G.

GN BONG.

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.

OX NCBI_Taxid=1491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=113 / 30;

RX MEDLINE=94092745; PubMed=8268233;

RA Campbell K., Collins M.D., East A.K.;

RT "Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium argentineense) type G neurotoxin: genealogical comparison with other clostridial neurotoxins."

RL Blochm. Biophys. Acta 1216:487-491(1993).

CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE.

CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.

CC -----

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CC -----

DR EMBL: X71162; CA52275.1; -.

DR HSSP: P10845; 3BTA.

DR MEROPS: M27.002; -.

DR InterPro: IPR000395; Bontolysin.

DR InterPro: IPR000130; Zn_metallopep.

DR Pfam: PF01742; Peptidase_M27.1.

DR PRINTS: PR00760; BONTOLYSIN.

DR ProDom: PD001963; Bontolysin; 1.

DR PROSITE: PS00142; ZINC_PROTEASE; 1.

DR Neurotoxin: Hydrolyase; Metalloprotease; Zinc.

FT INT MET 0 BY SIMILARITY.

FT CHAIN 1 441 BOTULINUM NEUROTOXIN G, LIGHT-CHAIN.

FT CHAIN 442 1296 BOTULINUM NEUROTOXIN G, HEAVY-CHAIN.

FT METAL 229 229 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 230 230 BY SIMILARITY.

FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).

FT DISULFID 435 449 INTERCHAIN (PROBABLE).

SO SEQUENCE 1296 AA; 149013 MW; DC8E47E15F65C31 CRC64;

Query Match 2.6%; Score 146.5; DB 1; Length 1296;

Best Local Similarity 18.2%; Pred. No. 0.29; Indels 313; Gaps 56;

Matches 196; Conservative 172; Mismatches 397;

43 KLM-ASAFGEIKSIAMKYSGLQKKYKKEKVAIEET-----DGLQLVKKLA 92

Db 345 KLYKALMGFTETNLAGEY-GIKTRYSESEYLPDIKTEKLLDNTIYQNEGFNIA-----S 400

Qy 93 KMEEMFHKKSFAVRVRLVDAEAEHLKH-----EPDADLOVEYF-----NALIERD-- 140

Db 401 KMLKEPFOONKAVNK--EAYEISELHLVIYRIAMCKRVMKNGKSEOCITVNNEDLE 458

Qy 141 ----KDGNFLELGEFIIAPNDHFNNLPVNISL-----SDVQV---TNNYKNDP 183

Db 459 FIANKDSFKDLAKETIATNTQNTTIENNFSIDQLIDNDLSSGIDLPENETPEFTND 518

Qy 184 AIVNGVWSES-LNKVPVNDNEDRPSLIWQVFGSAKGFERYQYGIKWEPPDENGVIAPDCR 242

Db 519 DIDIPVIYIKOSALKKIFVDG-----DSLFEYL-HAQTFPSNIENQLTNSLDALR--N 569

Qy 243 NKKWYIQATSPKDVIIIVDVSGSKGLRLTI-----AAQVYSILDTIGDDDF 291

Db 570 NKKVYTFPSTN-----LVKANTVYGASLFVNWVKYVIDFTSSTQSTIDKVS-- 620

Qy 292 FNIIVNEELHAYEPCLNGLTQADRTNKEHREHLD---KLPAKGIGMDIALNEAFN 347

Db 621 VSII-----IPYIGALN-----VGNETAKENKMFELGGAAILMEFIPELVPTVGFPT 671

Qy 348 ILSDFNHTGGSGISQALMLITDGAVDVDTIETARYNMPDRKRVLTFTYLIGREAAFDNL 407

Db 672 LESYGNKGH-----IIMTISNALKRRD-----QKMTD---MYGLIVS----- 706

Qy 408 KIMACANKGFTQISTLADVOENVMELHVLRS--PKYIDQEHVDVWVTEAYIDSTLTDDQ 465

Db 707 QMLSTVNTQFYT-----IKRMYNALNOSQALEKIIEDQYNNRSEBKNNINID--- 756

Qy 466 GPVLNTTVAAMPFSKONETRSKIGILGVGVD-----VPYKELLKTP 508

Db 757 -----FNIDFKRLNSILANNIDDFINQCSISYLNMRMPLAVKAKLKDD 804

Qy 509 KYKLIHGATPITNGGILTHPELRLLYEBGKRRKPNYSVDISEVEMEDRDVYLRNA 568

Db 805 MLKRLLEY--IDTIELYLL--DEVNIILSKVRNHLKOSI--PFDLS---LYTKDYLILQV 856

Qy 569 MVRKRTGFSMEVKTVQSKRVLYMT-----NNYYVDIGTFPSLGSVALSRGH 619

Db 857 FNNYISNINNAIILSLRSGHLIDSSGATMNVGSDVIFNDINQFKLNSEN----- 912

Qy 620 KYFFGNVYIEBG---LHDLHPDVSLADEMS-----YCNTDLPHERHLSQLEAI 667

Db 913 ----SNTFAHQSKRVYVD-----SMFDNFSINFWVRPKYNNND-----I 948

Qy 668 KLYLKGEPLOCKELIQLVLFDAVVSAPIEA---YTSIALNKSSENS----- 713

Db 949 QYVLQNETYTIISCIN-----DSGMWVYSIKGNRIIMTLIDVNAKSKSIFFEYSIKDNI 1001

Qy 714 ----DKGEVAFELGRTGSLRINLVGAEOQLNODFLAGDKENIFENDHPL----- 762

Db 1002 SDYINKWFSITTYNDRLG--NANIYIINSKKSEKILNL--DRINSSNDIDFKLINCTDTT 1058

Qy 763 ---W-----YRRAEQIPGSEFVSIPESTGPVKN--SNVYASTSIQDLDERKSPV-- 809

Db 1059 KFWVTKDFNINIGRELNATEVSSLYIGQSTNTLKPFGWGNPLKRYDQYVLLPQNGMQNIYIK 1118

Qy 810 -----AAVGIO---MKLEFQKRFATSHQCSLDGKCSISDD--- 845

Db 1119 YFSKASMGETAPRTNNAANAIYQNLVGLRLFIKK-----ASNSRINNDNTYVR 1168

Qy 846 ETVNGYL-IDN-----NGFLVSESDYOTQDGFGEI--EGAVMNKLLLMGSKRRTLLDY 897

Db 1169 EGDYIYLVINDISDESRYVYLVNKSKEITQTLFAPINDPPTFYDVLIDIKKYKETTYYNC 1228

Qy 898 QAMCRANKESSDGAHGL-----LDPYNAFLSAVKWIMTELVLVLFVEFNL--CSW 944

Db 1229 QILCKDKTKTF--GLFGICKFVKDGYVMDYTDNFCISQWTLRIRISENINRLRLGCMW 1285

RESULT 15

.....

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2002, 22:18:00 ; Search time 117.99 Seconds
(without alignments)
1590.809 Million cell updates/sec

Title: US-09-787-657-5
Perfect score: 5667
Sequence: 1 MAGPGSPRRASRGASALIAA.....SLQAQTVLLPLLMFSR 1085

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	5524	97.5	1091	11	Q921L5
2	5198	91.7	997	4	Q9NY16
3	2600	45.9	519	4	Q9NY18
4	1409.5	24.9	2190	5	Q9NK64
5	1394.5	24.6	2172	5	Q9VJM0
6	1382.5	24.4	1022	5	Q9V6T7
7	1376.5	24.3	1191	5	Q9VJN7
8	1374.5	24.3	1255	5	Q9NK83
9	1209.5	21.3	1150	4	Q9NY47
10	1209	21.2	1145	4	Q9NY48
11	1200	21.0	1076	4	Q9Y268
12	1188.5	20.9	1156	11	Q9E0G2
13	1183.5	20.8	1084	11	Q920H6
14	1181	20.6	1103	11	Q08532
15	1168.5	20.4	1091	11	Q9ERS3
16	1157.5	20.4	1091	11	Q9ERS3

17	1151.5	20.3	1091	6	077773	077773 sus scrofa
18	1134	20.0	1110	4	Q9NIU0	Q9NIU0 homo sapien
19	1093	19.3	975	4	Q9NSA6	Q9NSA6 homo sapien
20	987.5	17.4	842	5	Q95R75	Q95R75 drosophila
21	899	15.9	180	6	Q9GMY4	Q9GMY4 macaca fasc
22	678.5	12.0	745	4	Q9UDQ3	Q9UDQ3 homo sapien
23	561	9.9	1148	5	017517	017517 caenorhabdit
24	365	6.4	317	11	Q920H5	Q920H5 mus musculus
25	335.5	5.9	170	4	Q9UDL7	Q9UDL7 homo sapien
26	320.5	5.7	1185	4	Q9HCJ9	Q9HCJ9 homo sapien
27	206	3.6	1449	5	Q9V917	Q9V917 drosophila
28	203	3.6	1450	16	Q9CE07	Q9CE07 lactococcus
29	189	3.3	978	6	Q95KE0	Q95KE0 macaca fasc
30	178	3.1	100	6	Q9GLM1	Q9GLM1 bos taurus
31	163.5	2.9	886	11	Q91NC9	Q91NC9 mus musculus
32	162.5	2.9	223	11	Q9142	Q9142 mus musculus
33	161.5	2.8	1577	5	Q9NKC7	Q9NKC7 drosophila
34	159.5	2.8	946	6	Q9GLY6	Q9GLY6 oryctolagus
35	153	2.7	2166	16	051465	051465 borrelia bu
36	151.5	2.7	907	13	Q9PVP8	Q9PVP8 brachydanio
37	146	2.6	532	2	Q9LJ75	Q9LJ75 streptococ
38	145.5	2.6	3254	5	Q9BK45	Q9BK45 plasmodium
39	144.5	2.5	4081	5	Q9VWZ3	Q9VWZ3 drosophila
40	141.5	2.5	525	4	076057	076057 homo sapien
41	140.5	2.5	1159	2	P71109	P71109 clostridium
42	140	2.5	1387	5	Q9GZ76	Q9GZ76 plasmodium
43	139.5	2.5	903	6	Q9GLY5	Q9GLY5 oryctolagus
44	139.5	2.5	906	6	Q9TJ34	Q9TJ34 oryctolagus
45	139.5	2.5	1302	2	Q49547	Q49547 mycoplasma

ALIGNMENTS

RESULT 1
ID Q921L5 PRELIMINARY; PRT: 1091 AA.
AC Q921L5:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCIDIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Klugbauer N., Lactinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL: AJ010949; CA009423.1; -.
DR MGD: MGI:1338890; Caccna2d3.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VMFA.
DR Pfam: PF02743; Cache; 2.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWF_A; 1.
SQ SEQUENCE 1091 AA; 122777 MW; 7AE2BDAL10077A0A CRC64;

Query Match 97.5%; Score 5524; DB 11; Length 1091;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1064; Conservative 2; Mismatches 19; Indels 6; Gaps 1;

QY 1 MAGPGSPRRASRGASALIAALILYALGDVRSSEOIPISVYKWSARGGEIKTSIAAY 60
Db 1 MAGPGSLCCASRGASALIALTALYALGDVRSSEOIPISVYKWSARGGEIKTSIAAY 60
QY 61 SCSOLQKKRYEKDVATEEIDGLQVKKLAKNMEEMFHKRSEAVRRIVEAAEENLHK 120
|||||

Db 61 SGOLOKKKYEKEKDAIEEIDGLQVKKLAKIMEEHKKSSEAVRRLVEAEBAHLKH 120
OY 121 EFDADLOEYENAVLINERDKGNFLGKEPILAPNDHPNNLPVNISLSDQVPTNNYN 180
Db 121 EFDADLOEYENAVLINERDKGNFLGKEPILAPNDHPNNLPVNISLSDQVPTNNYN 180
OY 181 KDAIIVNGVWSESINKVFVNDPDRPSLIQWFGSAGFFRQYPGIWMEDENGVIKFD 240
Db 181 KDAIIVNGVWSESINKVFVNDPDRPSLIQWFGSAGFFRQYPGIWMEDENGVIKFD 240
OY 241 CRNKKWTIOAATSPKDVYILVDVSGSMGKRLTIAKQTVSSILDTLGDGDDFFNITAYNEE 300
Db 241 CRNKKWTIOAATSPKDVYILVDVSGSMGKRLTIAKQTVSSILDTLGDGDDFFNITAYNEE 300
OY 301 LHAYEPCNLGLVQADPTNKEHFRHLDBLKFAKIGMDILNEAFNILDENHTGQCSI 360
Db 301 LHAYEPCNLGLVQADPTNKEHFRHLDBLKFAKIGMDILNEAFNILDENHTGQCSI 360
OY 361 CSQAIMLTIDGAVDTYDTIFAKYNNPDRKVRIFTYLLIGREAFADNLKMACANKGFFTO 420
Db 361 CSQAIMLTIDGAVDTYDTIFAKYNNPDRKVRIFTYLLIGREAFADNLKMACANKGFFTO 420
OY 421 ISTLADVOENWEXLHVLSRKRVLDQEHVDVWTEAYIDST-----LTDGCPVLTMTVA 474
Db 421 ISTLADVOENWEXLHVLSRKRVLDQEHVDVWTEAYIDST-----LTDGCPVLTMTVA 474
OY 475 MPVFSKQNETRSKGLGCVGTDPVKELKTIPKYLGIHGAFAITNNGYILTHPELR 534
Db 475 MPVFSKQNETRSKGLGCVGTDPVKELKTIPKYLGIHGAFAITNNGYILTHPELR 534
OY 535 LLYEEGKKRRRPNVSSVDLSEVEMEDRDVLRNANVNRKTGKFSMEVKRYDKGRVLVW 594
Db 535 LLYEEGKKRRRPNVSSVDLSEVEMEDRDVLRNANVNRKTGKFSMEVKRYDKGRVLVW 594
OY 595 TNDVYTDIKCTPPSLGVALSRGHCKYFFRGVNTIEEGLHDLHEDVSLADEMSKCNLD 654
Db 595 TNDVYTDIKCTPPSLGVALSRGHCKYFFRGVNTIEEGLHDLHEDVSLADEMSKCNLD 654
OY 601 TNDVYTDIKCTPPSLGVALSRGHCKYFFRGVNTIEEGLHDLHEDVSLADEMSKCNLD 660
Db 601 TNDVYTDIKCTPPSLGVALSRGHCKYFFRGVNTIEEGLHDLHEDVSLADEMSKCNLD 660
OY 655 HPEHRHLSQLEAIKLYLKGEKPELLOCKEKLQEVLFDAVVSAPIPAYWTSIALNKSEMSD 714
Db 655 HPEHRHLSQLEAIKLYLKGEKPELLOCKEKLQEVLFDAVVSAPIPAYWTSIALNKSEMSD 714
OY 715 KGEVAFLGTRTGLSRINLFGAEOULTNODFLKAGDKENIFNADHPLMYRRAAEQIDGS 774
Db 715 KGEVAFLGTRTGLSRINLFGAEOULTNODFLKAGDKENIFNADHPLMYRRAAEQIDGS 774
OY 775 FVYSIIPSTGVNKSNNVTASTSTQILDERKSPVAAVGIOMLKLEFQRKFWTASROCAS 834
Db 775 FVYSIIPSTGVNKSNNVTASTSTQILDERKSPVAAVGIOMLKLEFQRKFWTASROCAS 834
OY 835 LDGKCSISDDEETVNCYLIDNNGFLVSEDTQNGDFGEIEGAVMNKLLTMGSPKRTTL 894
Db 835 LDGKCSISDDEETVNCYLIDNNGFLVSEDTQNGDFGEIEGAVMNKLLTMGSPKRTTL 894
OY 841 LDGKCSISDDEETVNCYLIDNNGFLVSEDTQNGDFGEIEGAVMNKLLTMGSPKRTTL 900
Db 841 LDGKCSISDDEETVNCYLIDNNGFLVSEDTQNGDFGEIEGAVMNKLLTMGSPKRTTL 900
OY 895 YDYOAMCRANKESSDGAGLLDPYNAFLSAVKWIMTELVLVLVEBNLCSMWSHSDMTAKAQ 954
Db 895 YDYOAMCRANKESSDGAGLLDPYNAFLSAVKWIMTELVLVLVEBNLCSMWSHSDMTAKAQ 954
OY 901 YDYOAMCRANKESSDGAGLLDPYNAFLSAVKWIMTELVLVLVEBNLCSMWSHSDMTAKAQ 960
Db 901 YDYOAMCRANKESSDGAGLLDPYNAFLSAVKWIMTELVLVLVEBNLCSMWSHSDMTAKAQ 960
OY 955 KLKQTLERCDTEYPAFVSEKRTIKETGNIACEDCSKSFVIOOIPSSNLFPMVWSSCCE 1014
Db 955 KLKQTLERCDTEYPAFVSEKRTIKETGNIACEDCSKSFVIOOIPSSNLFPMVWSSCCE 1014
OY 961 KLKQTLERCDTEYPAFVSEKRTIKETGNIACEDCSKSFVIOOIPSSNLFPMVWSSCCE 1020
Db 961 KLKQTLERCDTEYPAFVSEKRTIKETGNIACEDCSKSFVIOOIPSSNLFPMVWSSCCE 1020
OY 1015 SVAITMAPIRIRYNESLKCERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1074
Db 1015 SVAITMAPIRIRYNESLKCERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1074
OY 1021 SVAITMAPIRIRYNESLKCERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1080
Db 1021 SVAITMAPIRIRYNESLKCERLKAOKIRRRPESCHGHPENARECGGASLOAQVTL 1080
OY 1075 LPLLLMLFSR 1085
Db 1075 LPLLLMLFSR 1085
OY 1081 LPLVSSLSFR 1091
Db 1081 LPLVSSLSFR 1091

ID O9NY16 PRELIMINARY; PRF: 997 AA.
AC O9NY16;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 15, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21142395; PubMed=11245980;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272268; CAB75962.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; vWFA.
DR Pfam; PF02743; Cache: 2.
DR SMART; SM00327; vWFA; 1.
DR PROSITE; PS50234; vWFA; 1.
SQ SEQUENCE 997 AA: 112996 MW: 856D1313FD678BD CRC64;

Query Match 91.7%; Score 5198; DB 4; Length 997;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

OY 95 MEEMFHKKSEAVRRLVEAEBAHLKHEFDADLOEYFNAVLINERDKGNFLGKEPIL 154
Db 1 MEEMFHKKSEAVRRLVEAEBAHLKHEFDADLOEYFNAVLINERDKGNFLGKEPIL 60
OY 155 APNDHFNMLPVNISLSDQVPTNNYKDPALVNGVWSESINKVFVNDPDRPSLIQWYF 214
Db 61 APNDHFNMLPVNISLSDQVPTNNYKDPALVNGVWSESINKVFVNDPDRPSLIQWYF 120
OY 215 GSAKFFRQYPGIKWEPENGVIAFDCKRNKMYIOAATSPKDVYILVDVSGSMKRLRTI 274
Db 121 GSAKFFRQYPGIKWEPENGVIAFDCKRNKMYIOAATSPKDVYILVDVSGSMKRLRTI 180
OY 275 AKQTVSSILDTLGDGDDFFNITAYNEELHYVEPCLNGTVQADRTKKEHFRHLDBLKFAKG 334
Db 181 AKQTVSSILDTLGDGDDFFNITAYNEELHYVEPCLNGTVQADRTKKEHFRHLDBLKFAKG 240
OY 335 IGMIDLALNEAFNILDENHTGQGSICQAIMLTIDGAVDTYDTIFAKYNNPDRKVRIFT 394
Db 241 IGMIDLALNEAFNILDENHTGQGSICQAIMLTIDGAVDTYDTIFAKYNNPDRKVRIFT 300
OY 395 YLIGREAFADNLKMACANKGFFTOISTLADVOENWEXLHVLSRKRVLDQEHVDVWTE 454
Db 301 YLIGREAFADNLKMACANKGFFTOISTLADVOENWEXLHVLSRKRVLDQEHVDVWTE 360
OY 455 AYIDST-----LTDGCPVLTMTVAAMPVFSKQNETRSKGLLGAVGDPVKELKTIP 508
Db 361 AYIDST-----LTDGCPVLTMTVAAMPVFSKQNETRSKGLLGAVGDPVKELKTIP 420
OY 509 KYKLGINGAYARITNGYILTHPELRLLYEBGKKRRKPNVSSVDLSEVEMEDRDVLRNA 568
Db 421 KYKLGINGAYARITNGYILTHPELRLLYEBGKKRRKPNVSSVDLSEVEMEDRDVLRNA 480
OY 569 MYNRKTGFSMEVKKTVDKGRVLVMTNDYTTDKGTPSLGVALSGHCKYFFRGVNT 628
Db 481 MYNRKTGFSMEVKKTVDKGRVLVMTNDYTTDKGTPSLGVALSGHCKYFFRGVNT 540
OY 629 IEEGLHDLHEDVSLADEMSKCNLDLHPEHRHLSQLEAIKLYLKGEKPELLOCKEKLQEV 688
Db 541 IEEGLHDLHEDVSLADEMSKCNLDLHPEHRHLSQLEAIKLYLKGEKPELLOCKEKLQEV 600
OY 689 LFDVAVSAPIPAYWTSIALNKSENSDKGEVAFLGTRTGLSRINLFGAEOULTNODFLKA 748

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|||||
Db 601 LEADVAPAEIAYWTSALANKSENKDGVEAFLEGTGRLSLINLFVGAEOGLTNDFLKA 660
Qy 749 GDKREIFNADHPPLMYRRAAEOIPGSPFYIPIFSTGPVKNKSVVTAISTSIQLDERKSPV 808
Db 661 GKRENIIFNADHPPLMYRRAAEOIPGSPFYIPIFSTGPVKNKSVVTAISTSIQLDERKSPV 720
Qy 809 VAAVGIQKLEFFORKFMTASROCASLDGKCSISCDDEFVNCYLLIDNNCFILVSEDTYT 868
Db 721 VAAVGIQKLEFFORKFMTASROCASLDGKCSISCDDEFVNCYLLIDNNCFILVSEDTYT 780
Qy 869 GDFEIEIGAVANNKLLTNGSFKRITLYDQAMCRANKESSDGAHGLDYPNAFLSAVKVI 928
Db 781 GDFEIEIGAVANNKLLTNGSFKRITLYDQAMCRANKESSDGAHGLDYPNAFLSAVKVI 840
Qy 929 MTELVLFLVEFNLCGSMHSDMTAKAKQLKQLEPCDTEYPAFVSERTIKETGNACEDC 988
Db 841 MTELVLFLVEFNLCGSMHSDMTAKAKQLKQLEPCDTEYPAFVSERTIKETGNACEDC 900
Qy 989 SKSEFYIOIPSSNLFMVVDSCLCESVAPITMAPLEIRYNSLNCERLKAQIRRRPS 1048
Db 901 SKSEFYIOIPSSNLFMVVDSCLCESVAPITMAPLEIRYNSLNCERLKAQIRRRPS 960
Qy 1049 CHGFHPEENARECGAPSLQAOQTVLLPLMLFSR 1085
Db 961 CHGFHPEENARECGAPSLQAOQTVLLPLMLFSR 997

RESULT 3
Q9NY18 PRELIMINARY: PRT: 519 AA.
ID AC Q9NY18:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=21142395; PubMed=11245980;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL: AJ272213; CAB5878.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; VMA; 1.
DR PROSITE: PS50234; VWFA; 1.
SQ SEQUENCE 519 AA; 59526 MW; 198D13AF246286C6 CRC64;

Query Match 45.9%; Score 2600; DB 4; Length 519;
Best Local Similarity 99.8%; Pred. No.1.8e-165;
Matches 495; Conservative 0; Mismatches 1; IndeIs 0; Gaps 0;

Qy 95 MEMEHKSEARRLVEAAEHAHLKHEPDADIQEYFNANVLINERKGNFLELGKFFLL 154
Db 1 MEMEHKSEARRLVEAAEHAHLKHEPDADIQEYFNANVLINERKGNFLELGKFFLL 60
Qy 155 APNDHFNNLPVNIISLDVQVPTNMTNKDPAIANGVYVSESLKKEVDFNDRDPSLIMQYF 214
Db 61 APNDHFNNLPVNIISLDVQVPTNMTNKDPAIANGVYVSESLKKEVDFNDRDPSLIMQYF 120
Qy 215 GSAKGFPROYPGIKWEPDENGVIAFDCRRKKRYIOAATSPKDVILLVVGSMKGLRLTI 274
Db 121 GSAKGFPROYPGIKWEPDENGVIAFDCRRKKRYIOAATSPKDVILLVVGSMKGLRLTI 180
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Qy 275 AKOTVSSITLDTGGDDFFNINIAVNEELHYVEPLCNTLIVQADRTNKEHREHLDKFLFAG 334
Db 181 AKOTVSSITLDTGGDDFFNINIAVNEELHYVEPLCNTLIVQADRTNKEHREHLDKFLFAG 240
Qy 335 IGLMDLALNEAFNLSDFNHTGSGSICSOAIMLTIGAVDYTFIPAKYNMPDRKRIPT 394
Db 241 IGLMDLALNEAFNLSDFNHTGSGSICSOAIMLTIGAVDYTFIPAKYNMPDRKRIPT 300
Qy 395 YLIGREAPADNLKMAKANKGFTQISTLADVQENVMEYLHLSRPKYIDOEHDVWTE 454
Db 301 YLIGREAPADNLKMAKANKGFTQISTLADVQENVMEYLHLSRPKYIDOEHDVWTE 360
Qy 455 AYIDSLTLDQGGVLTMTYVAMPYFSKONETRSKGLLVGVGDVYPKELKTIPKYLGI 514
Db 361 AYIDSLTLDQGGVLTMTYVAMPYFSKONETRSKGLLVGVGDVYPKELKTIPKYLGI 420
Qy 515 HGAFATNNGYLLTPRELRLYEKGKRRKPNYSSVDLSEVEMEDRDVLRNANVRKT 574
Db 421 HGAFATNNGYLLTPRELRLYEKGKRRKPNYSSVDLSEVEMEDRDVLRNANVRKT 480
Qy 575 GKFSMEVKKTVDKGR 590
Db 481 GKFSMEVKKTVDKGR 496

RESULT 4
Q9NR64 PRELIMINARY: PRT: 2190 AA.
ID AC Q9NR64:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE HYPOTHETICAL 249.8 KDA PROTEIN.
GN BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Mitra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzeil G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesioika L., Doyle C.M.,
RA Fartan D.E., Galle R., Hummasti S.R., Kaira K., Kearney L., Kim E., Lee B.,
RA Houston K.A., Hummasti S.R., Kaira K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomtan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zietan L.L., Rubin G.M.;
RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003415; AAF44988.1; -
DR FlyBase: FBgn0028859; BG:DS07473.1.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; VMA; 1.
DR PROSITE: PS50234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;
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[illegible]

DR FlyBase; FBgn0033870; CG12295.

Matches 348; Conservative 203; Mismatches 393; Indels 219; Gaps 32;

OY 108 RLYAAEAAHLKHEFDADLYE-----YFNAVLINEPKDGNFLGKEFLIAPNDHF 160
 Db 115 RLMDASDAQALS--ELEGGAGAESPMGGOQHYNARINIEYNADCKLADGAMHDIRFRRF 173
 OY 161 NNLPRVNLSDVOVPTNMKNKDPAINGVYVSSSLNKVVDNDRDPSLIWQYFGSAGKF 220
 Db 174 ERLPRVNLSSLIIVPHGVDDDEPDVKSALOMSGHLDPLFONNLEODPALSMQYFGSSTGF 233
 OY 221 FROYPIKMEPD--ENGVIADFCDNRKRWYIOATSPKDVYILVDVSGSMGKLRTIKOT 278
 Db 234 LRRFPCTAMPPESSKSKLHDFRTHNMFOVAASSPKDMLILLDASSSKSPFDLCMAT 293
 OY 279 VSSILDTLGGDDFFNIAYNEELHYVEPCINGTLVQADRTNKEHFHRLDLKFAKIGML 338
 Db 294 AFNILDITGDDFVNLITFEEVVKTPYPCFKDMVRATPRNIDELKSAVAKIKQDIANF 353
 OY 339 DIALNEAFNLSDFNHTGGSICSAIMLITDCAVDYDTITFAKYNMPDRKVRIFTYLLIG 398
 Db 354 TACLEAFSLHRYKNOGAGSQCNOAIMLITESTESHKDVIKQYMPHPRVRIFTYLLIG 413
 OY 399 REAFAFDNLKWMACANKGFTQISTLADVOENMEYLHVSRRKVIDQ--EHDVYVTEAYI 457
 Db 414 SDSGSRNLDHMACSKNGFVQINDYDEARKVIDYALVAPRIMQADHPHMSFV 473
 OY 458 -----DSTLTDGQPLMTVTAPVYFSKONETRSKIGLVGVTDVPEKELTIP 508
 Db 474 AGKSGGLGRNS-----EYGRVLTVTSTPVDRRHNHSVRANLLGVGTDPDIEIRKVI 529
 OY 509 KTKLGHGAFATNNGYILTPRELRLYEGR--KRRPNYSSVDLSEVEDRD---562
 Db 530 OHLKGNGYSFIVDNNGRVLYHBDRLPRLDQANQYIDQKPKYASVDITELLETETEGNN 589
 OY 563 -----DYLRAVAVRKTGKFSMEVKTVDGKRVLTVMYNYXDIDIGTPSLG 611
 Db 590 NEPIETINKULLNEMRGMKPKGEGTEFTVMYHYDSKRTSTHRTKRTFGIEDTPETLA 649
 OY 612 VALSRGHGKXF-----RGNAV--IEEGLDLEHDPVSLADEWYSYN---TDL---654
 Db 650 IYLPKXGSHSEFYSGOEIRHSRNNVTEYFRGDMVRVHPD-----WYCYGNSVSDLEKE 703
 OY 655 -----HPEHR-----HISOLEAIKLYLK 672
 Db 704 RESSGYSRDOBPSPGSEEDVYRPSQPHNMHSGSNGNAPGSHFGSOHQSSQGR 763
 OY 673 GREPLDCKKELIQEVLFDPAVVSAPTEAVWTSIALNKSENSDG-----VEVFLGRIG 727
 Db 764 KAEPR--CDRALLQSLVRDMAMVTDGLDRNTGSSSGK--EDKQOQYOKFVAVATSFVATRS 821
 OY 728 LSRINLVGAEOULT-----NODFLKAGKENINADHFPLMYRRAEQ--IGSEFYYSI 779
 Db 822 LRLMIDHVRPEDTPEPHSESDNVRAMDTS-----WYKRAIDQHSVEDRSEFYSV 871
 OY 780 PRSTGVYKSN--VVTASTSIQDLDERKSPVAAVGSIOMKLEFFOKKFWTASQCSLDG 837
 Db 872 PGSGGAIKSNMTLYTASHAIFVEHGRHKAAGVAVGLQFQHDLSAKHFIITSACTGMTG 931
 OY 838 KCSISDDEEVNGLIDNNGFLLVSEDYQOTGDFGEIEGAVNNKLLTMSKFRITLXY 897
 Db 932 -KRTCASNLDCYVLDNNGSEVYITSEMEHTGKFGQIDGTINDSLDODRIVRATVND 990
 OY 898 QAMCRANKESSDGAHGLDPRYNALSAVWIMTELV-----LFLVFNLCSSMMHSDMT- 950
 Db 991 QCGCSADNPYTAAGILNP--NRIGS---WFFHLLALSAWMLSLPASPASIRAMPQREYTY 1046
 OY 951 -----AKAKLKQLEPCDTEY-----PAVY 971
 Db 1047 DNEDEVVVDNNYSDEYEFGENEYNNQVDOEMDEFPTTADVEYTTPPRQHKHGVPRFS 1106
 OY 972 SE-----RT-----IKETGNTIACEDCSKSFYIOQIPSNLPM 1004
 Db 1107 PDBHNAARCDLRTLYMLQPERLINOQGNPNLKGLTNGHVSGCEPFSVOKIPHSNLIL 1166

OY 1005 VVVDSGLCES----VAPITMAPIEIRYNESLKCERIKAKIRRRPESCHGFPEE--NAR 1059
 Db 1167 LVVDTLPCGSKQKDIERLEAGV---IGACSTRROGQEBESRRRRPKCNTYHPEELIEQ 1223
 OY 1060 ECGAPSLQAOYVLLPLLLML 1082
 Db 1224 QCGGSTLLHMSGVIVAHLLM 1246

RESULT 9
 ID 09NY47 PRELIMINARY; PRT; 1150 AA.
 AC 09NY47;
 DT 01-OCT-2000 (T-Emblrel. 15, Created)
 DT 01-OCT-2000 (T-Emblrel. 15, last sequence update)
 DT 01-DEC-2001 (T-Emblrel. 19, last annotation update)
 DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
 GN CACNA2D2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID;
 RA Klugbauer N.;
 RL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID;
 RA Hobom M., Dai S., Marais E., Lacinova L.;
 RT "Neuronal distribution and functional characterization of the calcium
 RT channel α 2delta-2 subunit".
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A251368; CAB86193.1; -.
 DR InterPro: IPR004010; Cache.
 DR InterPro: IPR002035; WFA.
 DR Pfam: PF02743; Cache; 1.
 DR SMART: SM00327; WFA; 1.
 DR PROSITE: PS50234; WFA; 1.
 SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AF573C CRC64;

Query Match 21.3%; Score 1209.5; DB 4; Length 1150;
 Best local similarity 29.9%; Pred. No. 5.7e-72;
 Matches 348; Conservative 218; Mismatches 453; Indels 145; Gaps 42;

OY 3 GCGSPRRAS--RGASALLAALLYALGDVRSQDIPLSVYKLNASAFGEIKSIK 59
 Db 30 GPGTRRPTSGPRPMLWLLPLRLAAPGASAVSFPQ--QHTMQHVARRLGEGVDGVMRI 87
 OY 60 YGSSQLQKKYKREKEDVALEIDIGLVKKLKNMEEMHKSEAVRRLVEAAEEAHILK 119
 Db 88 FGVGQDLRELYKDNRLFEVQENEPQVLKRVAGDIESLDRKVOALKRLADAENFQKA 147
 OY 120 HEFDADLYE--YFNAVLINE--RDKDGNFLGK-----EFLIAPNDHFNNLPVNIS 168
 Db 148 HRMODINKEEDIYYAKDADELDDPESEPEVSGASASTLRDIFDPN--FKN-KVNS 204
 OY 169 LSDVOVPTNMKNKDPAINGVYVSSSLNKVVDNDRDPSLIWQYFGSAGKFFROYPGIK 228
 Db 205 YAAVQIPTDLYKSGSTIINELNMTALENFEMRRQDPTLLMQVGSATGVTRYYPATP 264
 OY 229 WEDENGVIAFDGCRNKKWYIOATSPKDVYILVDVSGSMGKLRLTIAKQTVSSIIDTFLD 288
 Db 265 WRAPK--IDLYDVRRRPWWYIQGASSPKDWTIYDVSGVGLTLKLMKTSVCEMLDTLSD 323
 OY 289 DDFENIIAYNEELHYVEPCINGTLVQADRTNKEHFHRLDLKFAKIGMLDIALNEAFNI 348
 Db 324 DDYVNVASFERKQAPYS--CFT--HLVQANVRNKKVFEKAEVAGVAKGTGTYKKAFFEYAFDQ 381
 OY 349 LSDFNHTGGSICSAIMLITDCAVDYDTITFAKYNMPDRKVRIFTYLLIGREAAFDNLK 408

Db	382	LQNSNITRAN--CNKMMIMTEGDEBRVQDVEKXNMPPRIYRVTFESVGHANDYPLQ	439
Qy	409	WMACANKGFTTQISTLADVOENMYEHLVLSRPKY--DOEHVVWTEAYIDSTLTLDQ	466
Db	440	WMACANKGYFEIPLSIGAIININFOEVLADIGRPMVLAKGEAKQVOMTVYEDAL-----G	494
Qy	467	PVLMTTAMVVS-----KQNERKSGILLGVGVDPVKELKTIIPYKXIGHYA	518
Db	495	LGVLVTTLEPFLNITQDQGEKKNO-----LTLGVAGIDVALMDIKRLTPMTTLGANSYV	549
Qy	519	FAITNNGYIITHELRLLYEEGKKRRKPNYSSVDISEEWEEDRDVLENAWNRKTKFS	578
Db	550	FAIDNLNGYVLLHPLK---PQTNPREFVTLDFLAELEDEKKEIRSMIDGNKGNQI	606
Qy	579	MEVKKYTDKGRKVLMTNDYITTDIKGTFFPSIGVALSRGKGYFFRGVNTIE-----	630
Db	607	RTLVKSLDE-RYIDEVIRNTWPIRISTVYSLGLVLP-PYSFELYQANLSOOLQVKLRI	664
Qy	631	EGLDLE-----HPDVLSDENSYCNTPDHPHRLSOLE-AIKLYLKGKEPLQC	680
Db	665	SKLDPEFELPSPESGHFIAP-R-EYCK-DLMSDNNTEFLKFIILMEKVPIDSKQC	722
Qy	681	DKELIQEVLFD-AVVSAPLEAWYFSLTLAKKSENSDKGYEVAFLGRTGLSRINLFVGAQ	739
Db	723	NNFLHLMLIDTGTIOOLIVERVWRDOLL-----TYSLLAVEAATDGGITRFVPRKAED	777
Qy	740	LTNDFLAKDGKKEIFNADHFLMYRRAAEQJPGSFVYSIPRSTG---PVKSN---VYT	793
Db	778	WT-----ENBPENAS---FYRRSLDN-HGVYKPRQDALLNPLLENDYVGL	823
Qy	794	ASTSIQLDERRKSPVVAAGIQMKLEFFFORKKFWTAS-----RQASLDGKCSISCD	844
Db	824	VSTAVELSLGRRTLRPAVGVKTLDEMAKFKVLASNTHQDQKQIGP-NSHENDCE	882
Qy	845	--DETVCYLIDNNGFLVS---EDYTQIGDFPGELEGAVNMKLLTMASFKRITLYDQA	899
Db	883	VNNBDLLCVLIDGGELVYLSNQHMDQVGRFFSEVDATMLATLNNSPYRKESYDQA	942
Qy	900	MCRANKESSDGA--HGLLDPYNA-----FLSAVWIMTELVLFLVEFNLCSMWHSMT	950
Db	943	ACAQPPGNGINCAAPRGVYTVADVADFLNLAMWTSAAAMSLFOQLLGLIYH--SWQAD-P	999
Qy	951	AKAOKLKQTLPECDTEYPAFVSERTIKET-----TGNACEDCSSEVYIQDPS	999
Db	1000	AEAEGSEPERE-----SSCVMKQTOYFEGSYNAYSYNALIDCGCSRLFHAKQRLTN	1049
Qy	1000	SNLEPMVAVVSDSCAESVAPITMAPIEFLRHNESIKCERLKAOKIRRRPSCGHFHEEAR	1059
Db	1050	TNLLFVVAEKP-LCSQCEAGRLQKETHSDGPQCELVORPRIRRGFHICFDYNATEDTS	1108
Qy	1060	ECG-GAPSLAQVYLLPLLLML	1082
Db	1109	DCGRGASFPPLSLVSLQLLLL	1132
RESULT	10		
Q9NY48		PRELIMINARY; PRT; 1143 AA.	
AC	Q9NY48;		
DT	01-OCN-2000 (Tremblrel, 15, Created)		
DT	01-OCN-2000 (Tremblrel, 15, Last sequence update)		
DT	01-DEC-2001 (Tremblrel, 19, Last annotation update)		
DE	CALCIUM CHANNEL, ADPRA 2/DELTA SUBUNIT 2.		
GN	CACNA2D2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEART;		
RA	Klugbauer N.;		

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RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium
RT channel alpha2delta-2 subunit";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; vWFA.
DR Pfam; PF02743; Cache.1.
DR SMART; SM00327; vWFA.1.
DR PROSITE; PS50234; vWFA.1.
SQ SEQUENCE 1143 AA; 129085 MW; 492556C9919A0CE5 CRC64;

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Query Match	21.38	Score 1209	DB 4	Length 1143
Best Local Similarity	29.78	Pred. No. 6.1e-72		
Matches 344; Conservative 222; Mismatches 452;				
			Indels 140;	Gaps 41;

```

0Y      3 GGGSPRRRS --- RGSALLTAALLYAALGDVRRSQOPLSVYVKIKMAWASAFGEIKSIKAK 59
        ||| : | : | | | | | | | | | | | | | | | | : | : | : | : | : | : | : |
Db     30 GGTTRPRPGSRPRLMLLPLPLPLLAAGASAYSPFO --QHTMQWARLRDEOVGVKRI   87
        ||| : | : | | | | | | | | | | | | | | | | : | : | : | : | : | : | : |
0Y     60 YSGSOLLKKRYKEYEKDVAIEEIDLOLVKRLAKMMEEMFHKSSEAVRILEAAEEALK    119
        : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     88 FCGVOQLKEIYDKNRNLEVEOVENEPOKLVEKYAGGIESILDRKVOALRLADAAFNPOKA   147
        : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
0Y     120 HEFDADLOYE--YENAVLINE-RDKGNFELGK-----ETLAPDNHENNLPVNIS    168
        | : | : | : | : | | : | : | : | : | : | | | : | | | | | | | | | | |
Db     148 HRMOONIKEEDIVYYDAKADADELDPESEDVERGSKASTLRJDFIEDPN--FKN-KVNYS   204
        | : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : |
0Y     169 LSDVOVPNNMYKKDDAIYNGVYMSLSLKPFVANDRDDPSLIWOYFFSAKGFEFRYPGK    228
        : | : | | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     205 YAAVOIPDIDYKSTVINELNMTALELEVEMENRRDPOTLLMOVGFSATGTRYTPRP    264
        : | : | | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
0Y     229 WEPPDNGVIAFPDCRRNKRWYIQATSPKDVILVDVSGSMKGRLTIAQTVSILLDTLGD    288
        : | : | | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     265 WMAPRK-IDLYVRRRPWWYIOGSSPKMWIIVDVSGVSGTLTKLMTSVCDEMILDSI    323
        : | : | | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
0Y     289 DDFENIIAYNEBLHYVEPLNGTLVQADBRTNKEHRREHLDKLFANGIGMDIALNEAFNI   348
        | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db     324 DDYVVVASNEKAQBPVS-CFT-HLQOANRNKKVFKEVOCWAAGTTGYKAGFEYARDO    381
        : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
0Y     349 LSFDEHHTOGGSTCSOAIMLTIDGAVDTDJTFPAKNRMDBKRIRIFTYLIGREAFAADMJK 408
        | : | : | | : | | : | : | | | : | | | | | | | : | : | : | : | : | : |
Db     382 IONSNTITRAN-CNKMIMEFTDGEDRVODEFEKNMPKPRTVRTEFSVGQNYNVPTPLO   439
        | : | : | | : | | : | : | | | : | | | | | | | : | : | : | : | : | : |
0Y     409 WMACANKGFETOISFLADVOENMEZYLAHLSRPXY--DOEHADVMTAEAYIDSTLITDDOG   466
        | | | | | : | : | : | : | | | | | | | | | | | : | : | : | : | : | : |
Db     440 WMACANKGYFEIPISIGAIRINTGOEYLDVLGRPMVLAGEAKAOVMONTVEYDAL-----G 494
        | | | | | : | : | : | : | | | | | | | | | | | : | : | : | : | : | : |
0Y     467 PYLMTTVAMPVS-----KONETRSGILLGAVGTDVPYKELLKTTPKXKLGIRGYA    518
        | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db     495 LGLVYTGLPVFNLNQODGEGEKKNO----LILGWGIDVALNDIKRLTPNYTLCAFGV    549
        | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
0Y     519 FAITNNGYILTHPELRLLYEBCGKRKRKRPYSSVDLSYEWMBEDRDVLNAMNRKTKGPS    578
        | | | | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     550 FAIDLNGVYLLHPNLK---POTTNRREVUTDLFDLAELEDKEKEIRISMIDGNKGKHQI    606
        | : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : |
0Y     579 MEWKRTVVGKGRHVLTMTNDYYTDTIKGTPEFSLGVALSRHGKFYFRGNVTIEEGSHLDEH 638
        : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     607 RLTVASIDE-RVIDERTNRYTWPIIRSTNYSLGVLP-PYSFYEQAN-LSDOILOYKY    662
        : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : |
0Y     639 PUVSLADER-----SYCNMDLPHBRHNSOLF-AIKLYLKGEPLLOCCKELIQ    686
        : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     663 FEFLLPSSSESGBHFIAPREYK-DLNASDNTEFLKNFETELMKVTPDSKOCCNNFLH    721
        : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : |
0Y     687 EYLFP-AVYASAPIELAYWTSLANKSENSDKGVEAFELGRTGISINLFVEAGEOLTNDOF   745
        : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Db     722 NLILTDTGITQOLVERKVRDQDLN-----TSLAVFAATDGSITVFPNKAAEDMT----- 772

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OY 746 LKADCKENIFNADHFPPLVYRAAEQIPGSFYVSIPEFTG---PVNKS---VVTASTSIQ 799
DB 773 -----ENPEPFNAS-----FYRRSLDN--HGYYFKPPHQDALLRPLELNDYGIIVSTAVE 822
OY 800 LLDERSKSPVVAAGVIGOMLLEFFQKFWTAS-----ROCASLDGCSISCD--DETV 848
DB 823 LSLGRRTLRPAVVGKLDLEAMAERKFKVLASNRTHODOPKCGP-NSHCMDCEVNNBDL 881
OY 849 NCYLIDNNGFTLVS---EDYTQTGDFEGEIGAVNNKLLTMSFKRITLYVOAMCRANK 905
DB 882 LCVLIDGGFLVLSNQHOMQOVGRFSEVDANLMLALYNSFYTRKESYDQAACAP 941
OY 906 ESSGCA--HGLDPPYA-----FLSAVKIMTELVLFLVEFNICSMWSDMTAKAOKL 956
DB 942 PGNIGAPRGVFPVADFLNLAMWTSAAMSLFQOLLGLIYH--SWFOAD-PAEAEGS 998
OY 957 KOTLEPCOTEPVAFVSERTKET-----TGNACEDCSFYIQIIPSNLHV 1005
DB 999 PETNE-----SSCYMKOTQYFGSVASNAVNAITDCGNSCLFHAQRLTNLLFV 1048
OY 1006 VVDSCLCESVAPITMAPIEIRYNESLKERLKAOKIRRPESCHGFPEENARECG-CA 1064
DB 1049 VAEKP-LCSGCEAGRLLOKETHSDGPECCELVQRRYRGPHICDYATEDITSOCGKA 1107
OY 1065 PSLQAVYVLLPLLLML 1082
DB 1108 SFPPSLGVLVSLQLLLL 1125

RESULT 11
OY9268 PRELIMINARY: PRT: 1145 AA.
AC Q9Y268;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE KIA0558 PROTEIN.
GN KIA0558.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,
Mauna J.D.;
RT "Gene 26, a new candidate human tumor suppressor gene located in the
3p21.3 small cell lung cancer homozygous deletion region homologous to
a voltage gated calcium channel alpha 2/ delta subunit."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kaashaba V.,
Zabarovskiy E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
channel resides in the lung cancer critical region on 3p21.3."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRNIN;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro."
RL DNA Res. 5:31-39(1998).
DR EMBL: AF040709; AAC70914.1; -;
DR EMBL: AF042792; AAB96913.1; -;
DR EMBL: AB011130; BAA25484.1; -;
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; vMFA.

DR Pfam; PF02743; Cache: 1.
DR SMART; SM00327; vMA; 1.
DR PROSITE; PS0234; vMFA; 1.
SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;

Query Match 21.2%; Score 1200; DB 4; Length 1145;
Best Local Similarity 29.7%; Pred. No. 2.4e-71;
Matches 345; Conservative 223; Mismatches 447; Indels 148; Gaps 43;

OY 3 GPGSPRRAS---RGASALLAAALYALAGDVYRSQQLPLSVYKIMASAFGEIKSIKAK 59
DB 30 GGTGRRPTSGPPRLMLPLPLPLAAGASAFSPQ--QHTMGHARRLEQVGVKRI 87
OY 60 YSGSGLQKKYKEYEKDVAIEIDQLVKKLAKMEEMFHKSAVRVLEAEALIK 119
DB 88 FCGVQQLREIKRDNRLFEVQENEPKLYEKVAGIESLDRKVALRLADAENPQKA 147
OY 120 HEFDADQYE--YFNAVLINR-RDKGNFLELQ-----EFTLADNDFNNILPVNIS 168
DB 148 HRMQDNKEEDIVYYDAKADAEIDPDESEDYERGSKASTLRIDFIEDPN--FKN-KVMS 204
OY 169 LSDVQVPTNNMKNDAIYNGVYMSLKKVPYDNDRDPSSLIMQVFGSAKGFRRYPCIK 228
DB 205 YAAVQIPTDIYKGVTLINELNMTALENVEENRRDPDTLLMOVFGSATGVTRYPATP 264
OY 229 WEPDENGVAIEDCRNRKKNYIOAATSPKDVILVDSGSMKGLRTIAKQTVSSIIDTGD 288
DB 265 WRAPKK-IDLYDVRRRRPYIGCASSPKDMVITVDVSGSVGLTLKMTSVCEMLDITSD 323
OY 289 DDFENIAYNEELAYVEPCLNGTVQADRTNKEHREHLDKLFAKGIMLDIALNEAFNI 348
DB 324 DDYVNVASFNEKAQPV-S-CFT-HLVQANVRNKKYKEKAVQGVAKGTGYKAGFEYADQ 381
OY 349 LSDENHTQGSICSAIMLIDGAVDTDTIFAKNMPDRVRIETVYLIGREARADNLK 408
DB 382 LQNSITRAN--CNKIMAFDGGEDRVQDVFEKKNMPRTVRFVTSVGQNNVDYPLQ 439
OY 409 WMAANKGFTFOISTLADQENVMELVLSRPKY--DOEHVYVWTEAVYIDSTLTDDG 466
DB 440 WMAKNKKYFEIPEIGAIRINTQGLDVLGRPNVLAKKAKQVMTVYEDAL-----G 494
OY 467 PVLMTVAMPVPS-----KQNETRSKGIILGVGTVDPYKELTKIPYKKGIGHYA 518
DB 495 LGLVVTGTLPEFNLQDQDPERKKNQ----LILGWGIDVVALNDIKRTPNVTLANGVY 549
OY 519 FAITNNGYILHRELRLILYEGKKRRKRPYSSVDLSEVEMEDRDVILNANVRRTGFS 578
DB 550 FAIDLNGVLLHLPNK--POTTNREPVTLDFDLAELEDEKKEIRKSMIDGNKHQOI 606
OY 579 MEVKTVYKGRVLMVMTNDYYTIDIKTPFSIGVALSGHKKYFPRGVTIEGLHLEH 638
DB 607 RTLVKSLDE-RYIDEVTNTYTWVPIRSTNYSGLVLP-PYSGFYQAN--LSDQTLQYK 662
OY 639 PDVSLADEW-----SYCNTDLHPEHRHLSQLE-AIKLYIKGEPLLOCKDELIQ 686
DB 663 FEELLPSFSEEGHFIAPREYCK-DLNASDNTEFLKNEFTELMKVPYPSDKQCNFFLH 721
OY 687 EYVLD-AVYSAPIEAWYSIALNKSNSDKGVAFVLCTRGLSINLFPVGAEOITNDNF 745
DB 722 NLIDTGTITQOLVERVWHDQDLN---TYSLLAVFAATDGTITRVFPNKAEDPT---- 772
OY 746 LKADCKENIFNADHFPPLVYRAAEQIPGSFYVSIPEFTG---PVNKS---VVTASTSIQ 799
DB 773 -----ENPEPFNAS-----FYRRSLDN--HGYYFKPPHQDALLRPLELNDYGIIVSTAVE 822
OY 800 LLDERSKSPVVAAGVIGOMLLEFFQKFWTAS-----ROCASLDGCSISCD--DETV 848
DB 823 LSLGRRTLRPAVVGKLDLEAMAERKFKVLASNRTHODOPKCGP-NSHCMDCEVNNBDL 881
OY 849 NCYLIDNNGFTLVS---EDYTQTGDFEGEIGAVNNKLLTMSFKRITLYVOAMCRANK 905
DB 882 LCVLIDGGFLVLSNQHOMQOVGRFSEVDANLMLALYNSFYTRKESYDQAACAP 941

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OY 906 ESSDGA--HGLIDPYNA-----FLSAVKWIMTELVLFLVEFNLCSSWMSHDMTAKAOKL 956
Db 942 PGNLDAABRGVFPVPAVDFNLAMWTSAAMSLFQOOLYGLYH--SWQAD-PAAEAGS 998
OY 957 KOTLEPCDTEYPAFVSERTIKET-----TGNACEDCSKSFVIOQIPSSNLFVW 1005
Db 999 PETRE-----SSCVMKOTQYFFGSVNASYNAIIDCGSCRLFHQRLNTNLLFV 1048
OY 1006 VVDSCL--CES---VADITMAPIEIRNESICKERLKAOKITRRPES-CHGFHPEENARE 1060
Db 1049 VAEKPLSCQCEAGRLQKETHCPAD---GPEQCELVORPRYRRGPHICFDYNATEDTSD 1104
OY 1061 CG-GAPSLQAQTVLLPLLLML 1082
Db 1105 CGRGASPPPSLGLVLSQLLLLL 1127

RESULT 12
OQUEMO PRELIMINARY: PRT: 1076 AA.
AC OQUEMO:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zadorovskiy E., Johnson B., Lerman M.I.;
RA "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3.";
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF042793; AAB96914.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; vMFA.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; vMA; 1.
DR PROSITE: PS50234; vMFA; 1.
SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CR64;
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OY 394 TYLIGREAAEADNLKMKACANKGFPTQISTLADVOENVMEYLVSAPKV--DQEHNV 451
Db 356 TFSVGGHNDVDFPLQWMAACNKGYFEIPSIGAIRINTQYLDVLGPPVLAKEAKQVO 415
OY 452 WTEAYIDSTLTDGQVPLMTTMAPVES-----KONETRSKGLLGVGTDVPEKL 503
Db 416 WTVNYEDAL-----GLGLVYTGTLPPFNLTQDPGKKNG-----LLTGMGIDVALNDI 465
OY 504 LKTIPIYKLGIGHYAPATNGYILTHPELRLLYEEGKKRRKNYSVDLSEVEMEDRD 563
Db 466 KRLTPVYTGANGYVAIDNGYVLLHPNLK---PQTNREPVTLDFDLAEAEDEKKEE 522
OY 564 VLPNMAVNRKTKGFSMEVKKTVDKGRVLMNTDYITDQKPPPSLGVALSNGHKYFE 623
Db 523 IRRSMIDGKNKGHOKITLVKSLDE-RYIDEVTNRVWPVIRSTNYSLGLVP-PYSTFYL 580
OY 624 RGNVTIEGLHDEHPDVSLADEM-----SYCNTDLPEHRHLSOLE-AIKLYL 671
Db 581 QAN--LSDQILQYKFEFLLPSSFESEGHVFIAPRECK-DLNASDNTEFLKNFIELME 637
OY 672 KGEPLLOCDKELIQEVLVD-AVVSAPTEAYWTSIALNSSENSDKGEVAFLCTPTGLSR 730
Db 638 KVPDPSKQCNFLHMLIIDTGITQOLVERWRDODLN---TSLAVFAATDGGITR 692
OY 731 INFVGAEOULTNODFLKAGDKENIFNADHPPLMYRRARAEOIPGSFYSTPFGS---PVN 787
Db 693 VEPNKAAEWMT-----ENPEPFNAS---FYRSLDN--HGYYFKPPHODALLRPE 738
OY 788 KSN---VVTASTISQLDERKSPVVAVGMIKLEFFORFKWTAS-----ROCASTL 835
Db 739 LENDTYGILVSTAVELSLGRRTLRPAVGVYKLLDEMAEKFYLAISRTQDPQKCGP- 797
OY 836 DGKCSISCD--DETVNCYLIDNNGFTLVS--EDYTQTDGFEGEIGAVANKLLTMGSEK 890
Db 798 NSHCENDCEVNNEDLCVLLDDGFLVLSNQNHQMPQVGFSEVDANLMLALYNNFSYT 857
OY 891 RITLYDQAMCRANKRESSDGA--HGLIDPYNA-----FLSAVKWIMTELVLFLVEFN 941
Db 858 RKESYDYQAACAPDPGNLGAARGVFPVPAVDFNLAMWTSAAMSLFQOOLYGLYH- 916
OY 942 CSMWMSDMTAKAOKLKOTLEPCDTEYPAFVSERTIKET-----TGNACEDCSK 990
Db 917 -SWFQAD-PAAEAGSPETRE-----SSCVMKOTQYFFGSVNASYNAIIDCGCSR 964
OY 991 SFVYIQIPSSNLFVVDSSCL--CES---VADITMAPIEIRNESICKERLKAOKITRR 1045
Db 965 LFAHQRLTYTNLLFLVAEKPLCSQCEAGRLQKETHCPAD---GPEQCELVORPRYRRG 1020
OY 1046 PESCHGFHPEENARECG-GAPSLQAQTVLLPLLLML 1082
Db 1021 PHICFDYNATEDYSDCGRGASPPPSLGLVLSQLLLLL 1058

RESULT 13
OQUEMO PRELIMINARY: PRT: 1156 AA.
AC OQUEMO:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2-DELTA-2 SUBUNIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=TKDU;
RC MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "Genomic organization of the mouse and human alphazdelta2 voltage-
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QY	274	IAQTVSSIIIDTLDGDDFFIIIAVNEELHAYVEPCLNGTLVQADRRNKEHFEHDLKFAK	333
Db	240	LMKTSVCEMLDITSDDDYVNVASFENKAPVS-CFT-HLYQAVNRKKVYFKFEAAQGVAK	297
QY	334	GIGMLDIALNEAFNIIISDFHNTGSGISGOA:IMLITDGAVDVYDIFPAKYMMPRKVAIF	393
Db	298	GTTGYKAGFEYAFDQLOANSITPAN--CNKIMIMTLDGEDRVQDYVEKYNMPPRYAVF	355
QY	394	TYLIGREAAFNLIKWMACANKGFTQISTLADVOENWEXYHLVSRPKVI--DOEHNV	451
Db	356	TFVSGHNYDVDTPLQWMACTNGKYFEIPEISGAIRINTQGEYLDVGRBMVLAKDAQVQ	415
QY	452	WTEYAVIDSTLDQGPVLMVTYAMPFS-----KQNEIRSKIIILJGVGTDPVKEL	503
Db	416	WTNYVEPAL-----GGLVYVTGLPFPENLTQDGPBEKKNQ-----LIIJVGIDVALNDI	465
QY	504	LKTPKFKLGHGAFAFNTNGVILIHPELRLIYEGCKRRKPNYSVDSLEVEDMD-	562
Db	466	KRLTPNTLVANGYVRAIDLNGVYLHPMLK--PQTTNFRFP--VTIDFIDALEIDENK	520
QY	563	DVLNMAVNRKGT-KESMEYKAVTDKGVVLVMTDYDTTIDKGTPEISGVALSGHKY	621
Db	521	BEIRSMIDDKGHQKQRLTVKSLDE-RVIDEYINVTWVPIRSINYSGLGLVP-PYSTY	578
QY	622	FFRGNTVIEGLHDLDEHPDVSLAD-----EMSYCNFTDLHPEHRHLSQ	663
Db	579	YLQAN--LRQIIQVLYPIISKLDPEFLPSSFESBGHFIAPREKY--DINASNSTEF	635
QY	664	L-EAIKIKYLLKGKEPLLOQCKELQOEVLDP-AVVASPIEAHWISLALNKSNSDKGVFAF	721
Db	636	LKQDTELMKVTYPDSCQKNFELHNLITDGTQOOLVERWMDQDLN----TYSLAVF	690
QY	722	LGTPTGLSRINLEFVGAEOITNODFLKAGDENIFNADHPELMYRRAAEQIGSFVYSIF	781
Db	691	AATDGGITRVFPPKAEDWT-----ENPEFPNAS-----PYRSLSLN--HGTYIFKPH	736
QY	782	STG---PVKSN--VVTASTSIQLDERKSPVAAVGIQMKLEFFQKKWTAS-----	829
Db	737	QDSILRLPELENDTVGVLVSTAVEISLGRRTLRPAVGVKIDLEAMAKFPVLSNRTHQ	796
QY	830	---RQGSALDGKSGISGD--DETVCNYLIDNNGFILVS---EDTYQTDGDFEGELIGANMN	881
Db	797	DQPKCCP-SSHCHEMDEVANNEDLCVLLIDDGFPVLNQNHQWQVGRFSEVDANLML	855
QY	882	KILMGSEFKRITTYLQVQAMCRANKESSDGA--HGLLDPYNA-----FLSAVKWIMTEL	932
Db	856	ALVYNSYTTKKESTVDQACAPQPPNGLCAARGVVPPIADFLMLAMVTSAAHNSFLQQ	915
QY	933	VLFVLEFNLCSMWHSMDTAKQKLTQLEPCDTEYPAFVSETIKET-----TG	981
Db	916	LLYGLIYH--SMFPQD-PAAEAGSPETRE-----SSCVMKQTVYFGSVNAYSNA	962
QY	982	NIAECDSKSFVIOQIPSSULFWVYVDDSSL--CES---VAFITMAP:FEIRNSLACER	1036
Db	963	IIDGNCNSRLFHQRLNTLNTLFFVAEKPLGSCQCEAGRLLOKRETHCPAD---GPEOCEL	1018
QY	1037	LKAQIKRRPESCHGFPEENARECG-GAPSLQAOVYLLPLILML	1082
Db	1019	VQPRRYRGRPHICEDYNATEDITSDCGRGASFPSPSLGVLVSLDILLLL	1065
RESULT 15			
008532			
ID	008532	PRELIMINARY: PRT: 1103 AA.	
AC	008532: 008533: 008534: 008535: 008536:		
DT	01-JUN-1998 (Tremblrel. 06, Created)		
DT	01-JUN-1998 (Tremblrel. 06, last sequence update)		
DT	01-OCT-2001 (Tremblrel. 18, last annotation update)		
DE	DIHYDROPIRINDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA		
DE	SUBUNITS PRECURSOR		
GN	CACNA2D1 OR CACNA2.		
OS	Mus musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

ID	Gene	Accession	Protein	Length	Score	DB
CC	Mammalia; Eutheta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
ON	NBLTaxid=10090;					
RM	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-BRAIN:					
RX	MEDLINE=97113514; PubMed=8955374;					
RA	Angelotti T., Hofmann F.;					
RL	FEBE Lett. 337:331-337(1996).					
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE					
CC	- EXCITATION-CONTRACTION COUPLING.					
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNIT					
CC	ALPHA-1', ALPHA-2, BETA AND GAMMA.					
CC	- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE					
CC	LINKED.					
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E					
CC	ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE					
CC	SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.					
CC	- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE					
CC	AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D I					
CC	EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN					
CC	SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE					
CC	CARDIOVASCULAR SYSTEM.					
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED F					
CC	A PRECURSOR FORM.					
CC	- SIMILARITY: TO OTHER SPECIES ALPHA-2 SUBUNIT.					
DR	EMBL; U73484; AAB50139.1; -					
DR	EMBL; U73485; AAB50140.1; -					
DR	EMBL; U73483; AAB50138.1; -					
DR	EMBL; U73486; AAB50141.1; -					
DR	EMBL; U73487; AAB50142.1; -					
DR	MGI; MGI:88295; Caccna2d1.					
DR	Interpro: IPR004010; Cache.					
DR	Interpro: IPR002035; WVFAs.					
DR	Pfam; PF02743; Cache; 1.					
DR	Pfam; PF00092; WVA; 1.					
DR	SMART; SM00327; WVA; 1.					
KW	PROSITE: PS50234; WVFAs; 1.					
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;					
KW	Alternative channel; Glycoprotein; Phosphorylation; Signal;					
KW	Alternative splicing.					
FT	SIGNAL	1	24	POTENTIAL.		
FT	CHAIN	25	957	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT		
FT	FT CHAIN	958	1103	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.		
FT	TRANSMEM	446	469	POTENTIAL.		
FT	TRANSMEM	918	942	POTENTIAL.		
FT	TRANSMEM	1079	1098	POTENTIAL.		
FT	MOD_RES	501	501	PHOSPHORYLATION (BY CAPK) (POTENTIAL)		
FT	FT MOD_RES	845	845	PHOSPHORYLATION (BY CAPK) (POTENTIAL)		
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	324	324	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	348	348	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	475	475	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	604	604	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	613	613	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	625	625	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	781	781	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	824	824	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	888	888	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	895	895	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	985	985	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	998	998	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	VARSPLIC	531	549	MISSING (IN ISOFORMS 2B AND 2E).		
FT	VARSPLIC	531	554	MISSING (IN ISOFORMS 2C AND 2D).		
FT	VARSPLIC	644	644	y -> SKGKMD (IN ISOFORMS 2A, 2D AND 2E).		
SO	SEQUENCE	1103 AA;	124629 MW;	103773BA73512004 CRC64;		

Query Match 20.6%; Score 1168.5; DB 11; Length 1103;
Best Local Similarity 28.7%; Pred. No. 2.9e-69;

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